

NOVEL SMALL PROTEINS, POLYNUCLEOTIDES ENCODING
THEM AND METHODS OF USING THE SAME

RELATED APPLICATIONS

This application claims priority to U.S.S.N. 60/243,642, filed October 26, 2000;
5 U.S.S.N. 60/243,320, filed October 26, 2000; U.S.S.N. 60/243,592, filed October 26, 2000;
U.S.S.N. 60/243,681, filed October 27, 2000; U.S.S.N. 60/243,863, filed October 27, 2000;
U.S.S.N. 60/244,443, filed October 31, 2000; U.S.S.N. 60/245,029, filed November 1, 2000;
U.S.S.N. 60/244,995, filed November 1, 2000; U.S.S.N. 60/245,293, filed November 2, 2000;
U.S.S.N. 60/245,315, filed November 2, 2000; U.S.S.N. 60/245,316, filed November 2, 2000;
10 U.S.S.N. 60/262,994, filed January 19, 2001; U.S.S.N. 60/269,056, filed February 15, 2001,
U.S.S.N. 60/272,923, filed March 2, 2001, U.S.S.N. 60/276,565, filed March 15, 2001, and
U.S.S.N. 60/318,119, filed September 17, 2001 each of which is incorporated by reference in
its entirety.

FIELD OF THE INVENTION

15 The invention relates to polynucleotides and the polypeptides encoded by such
polynucleotides, as well as vectors, host cells, antibodies and recombinant methods for
producing the polypeptides and polynucleotides, as well as methods for using the same.

BACKGROUND OF THE INVENTION

20 The present invention is based in part on nucleic acids encoding proteins that are new
members of the following protein families: Calpain-like, Epsin-like, Low Density Lipoprotein
B-like, purinoceptor-like, CG8841-like, Synaptotagmin-like, Serine Protease TLSP-like,
Glypican-2 Precursor-like, Mitogen-activated protein kinase kinase-like, Zinc finger protein
276 C2H2 type protein and Thymosin beta10-like. More particularly, the invention relates to
nucleic acids encoding novel polypeptides, as well as vectors, host cells, antibodies, and
25 recombinant methods for producing these nucleic acids and polypeptides.

Calpains are intracellular cysteine proteases that are regulated by calcium. They are
known to be involved in a number of cellular processes, such as apoptosis, protein processing,
cell differentiation, metabolism etc. As such, their role in pathophysiologies extends to - but is
not restricted to - tissue remodeling and regeneration (in response to a variety of injury models
30 in the eye, brain, spinal cord, kidney etc.), fertility, tumorigenesis and myopathies. One of the
genes identified in susceptibility to type II diabetes is a calpain (calpain-10) (Horikawa et al.,

Nat Genet 26(2):163-75, 2000). Polymorphisms within this gene are correlated with insulin resistance. Therapies targeting calpain are relevant to disease areas such as cataract, spinal cord injury, Alzheimer's disease, muscular dystrophy, acoustic trauma, diabetes, cancer, learning and memory defects and infertility. Knockout and transgenic models of various calpains also point to a potential role for this family of proteases in a number of cellular and disease processes.

Epsins are a family of proteins that bind to ENTH domain proteins such as Eps15. They are involved in clathrin-mediated endocytosis as well as intracellular protein sorting. Some members of this family undergo phosphorylation during mitosis. In addition, epsins are involved in endocytosis at synapses to compensate for secretion of neuro-transmitter containing vesicles. The interaction of epsin 1 with a transcription factor (promyelocytic leukemia zinc finger protein) has recently been demonstrated, making it likely that the endocytotic machinery can cross-talk with nuclear function. Perturbation of epsin function can lead to defects in the endocytosis of membrane receptors as well as secreted proteins like transferrin, with consequent side-effects. Defects in epsin may potentially lead to aberrant cell-cell signalling, developmental defects, aberrant neurotransmitter signalling etc.

Low density lipoprotein (LDL) particles are the major cholesterol carriers in circulation and their physiological function is to carry cholesterol to the cells. In the process of atherogenesis these particles are modified and they accumulate in the arterial wall. Elevated serum cholesterol bound to low density lipoprotein (LDL) is a characteristic of familial hypercholesterolemia. Individuals with coronary artery disease have a significantly higher mean lipoprotein concentration than those without coronary heart disease, suggesting that lipoprotein measurements may help predict the risk of coronary heart disease in individuals with familial hypercholesterolemia.

Many cells express plasma membrane receptors for extracellular molecules, termed purinoceptors, which appear to be coupled to a plasma membrane pore. Purinoceptors are primitive, widespread and serve many different systems. There are several subclasses of purinoceptors; receptors for adenosine (P1-purinoceptors) and receptors for ATP (P2-purinoceptors). As for other major transmitters such as acetylcholine, GABA, glutamate and 5-HT, receptors of two major families are activated by ATP, one (the P2X-purinoceptor family) mediates fast responses via ligand-gated ion channels, while the other (the P2Y-purinoceptor family) mediates slower responses via G-proteins.

Synaptotagmins (Syts) are brain-specific Ca^{2+} /phospholipid-binding proteins (Li et.al., Nature 375(6532):594-9, 1995). In hippocampal synapses, Syt I is essential for fast Ca^{2+} -

dependent synaptic vesicle exocytosis but not for $\text{Ca}(2+)$ -independent exocytosis. In vertebrates and invertebrates, Syt may therefore participate in $\text{Ca}(2+)$ -dependent synaptic membrane fusion, either by serving as the Ca^{2+} sensor in the last step of fast $\text{Ca}(2+)$ -triggered neurotransmitter release, or by collaborating with an additional Ca^{2+} sensor. While Syt I binds Ca^{2+} (refs 10, 11), its phospholipid binding is triggered at lower calcium concentrations (EC₅₀ = 3-6 μM) than those required for exocytosis. Furthermore, Syts bind clathrin-AP2 with high affinity, indicating that they may play a general role in endocytosis rather than being confined to a specialized function in regulated exocytosis. Here we resolve this apparent contradiction by describing four Syts, three of which (Syt VI, VII and VIII) are widely expressed in non-neural tissues. All Syts tested share a common domain structure, with a cytoplasmic region composed of two C2 domains that interacts with clathrin-AP2 (K_d = 0.1-1.0 nM) and with neural and non-neural syntaxins. The first C2 domains of Syt I, II, III, V and VII, but not of IV, VI or VIII, bind phospholipids with a similar $\text{Ca}(2+)$ -concentration dependence (EC₅₀ = 3-6 μM). The same C2 domains also bind syntaxin as a function of Ca^{2+} but the $\text{Ca}(2+)$ -concentration dependence of Syt I, II and V (> 200 μM) differs from that of Syt III and VII (< 10 μM).

Proteolytic enzymes that exploit serine in their catalytic activity are ubiquitous, being found in viruses, bacteria and eukaryotes. They include a wide range of peptidase activity, including exopeptidase, endopeptidase, oligopeptidase and omega-peptidase activity. Over 20 families (denoted S1 - S27) of serine protease have been identified, these being grouped into 6 clans (SA, SB, SC, SE, SF and SG) on the basis of structural similarity and other functional evidence. Structures are known for four of the clans (SA, SB, SC and SE): these appear to be totally unrelated, suggesting at least four evolutionary origins of serine peptidases and possibly many more. Notwithstanding their different evolutionary origins, there are similarities in the reaction mechanisms of several peptidases. Chymotrypsin, subtilisin and carboxypeptidase C clans have a catalytic triad of serine, aspartate and histidine in common: serine acts as a nucleophile, aspartate as an electrophile, and histidine as a base. The geometric orientations of the catalytic residues are similar between families, despite different protein folds. The linear arrangements of the catalytic residues commonly reflect clan relationships. For example the catalytic triad in the chymotrypsin clan (SA) is ordered HDS, but is ordered DHS in the subtilisin clan (SB) and SDH in the carboxypeptidase clan (SC).

Glypicans are a family of heparan sulfate proteoglycans that are anchored to the plasma membrane via a glycosylphosphatidylinositol modification. The six glypican genes identified so far show distinct developmental and tissue expression patterns in mice. Glypicans

could potentially also be secreted away from the membrane by proteolysis and the soluble protein could potentially act as a dominant-negative inhibitor of the intact protein. This family of proteins has been implicated in neuronal development, guidance and regeneration. It may thus have a role in synaptic plasticity. One of the glypican genes in *Drosophila* is involved in the wingless and decapentaplegic signaling pathways. Deficiencies in glypican-3 in mice lead to a congenital overgrowth syndrome. In humans, deletions and translocations involving the glypican-3 gene have been associated with an X-linked recessive gigantism syndrome. In addition, the expression of this protein is silenced in an in vitro model of malignant mesothelioma. The novel protein, therefore, may play a role in tissue morphogenesis and patterning, cell division and cell signaling.

Mitogen-activated protein kinase kinase (MAPKK) is a dual-specificity protein kinase which phosphorylates and activates mitogen-activated protein kinase (MAPK). cDNAs encoding two isoforms of MAPKK, MAPKK1 and MAPKK2 (also known as MEK1 and MEK2), have been cloned in mammalian cells (Moriguchi et al., *Eur J Biochem* 234(1):32-8, 1995). Mitogen-activated protein kinase kinase 1 (MAPKK1) and MAPKK2 function downstream of the proto-oncogene product Raf in signaling pathways that affect cell proliferation and differentiation. The isoforms have been shown to be differentially regulated in two significant ways: MAPKK1, but not MAPKK2, was phosphorylated and inactivated by the cyclin-dependent kinase p34cdc2; and p21 Ras formed a ternary complex with Raf/MAPKK1 but not with Raf/MAPKK2 (Mansour et al., *Cell Growth Differ* 7(2):243-50, 1996). In a study of mouse tissues, MAPKK1 was shown to be highly enriched in the brain while MAPKK2 is present relatively evenly. Both isoforms were shown to reside in the cytoplasm and both are activated in response to nerve growth factor (NGF) and epidermal growth factor (EGF) (Moriguchi et al., *Eur J Biochem* 234(1):32-8, 1995).

A startling number of cDNA clones encode proteins that contain one or more sequences that match the zinc finger consensus domain, revealing that zinc finger proteins represent perhaps the largest class of DNA binding proteins in eukaryotes and that zinc finger protein-controlled gene expression may be a fundamental aspect of development as well as other processes. Structurally distinct clusters of zinc finger modules define an extremely large superfamily of nucleic acid binding proteins with several hundred, perhaps thousands of different members in vertebrates. C2H2 type zinc finger proteins (ZFPs) are one of the most complex members of zinc finger modular (Pieler et al., *Mol Biol Rep* 20(1):1-8, 1994 and Berg et al., *Annu Rev Biophys Biophys Chem* 19:405-21, 1990).

The beta-thymosins comprise a family of structurally related, highly conserved acidic polypeptides, originally isolated from calf thymus. A number of peptides belong to this family. They include, thymosin beta-4 is a small polypeptide that was first isolated as a thymic hormone and induced terminal deoxynucleotidyltransferase, thymosin beta-9 (and beta-8) in bovine and pig, thymosin beta-10 in man and rat, thymosin beta-11 and beta-12 in trout and human Nb thymosin beta. They found in high quantity in thymus and spleen but are also widely distributed in many tissues. They have been shown to bind to actin monomers and thus to inhibit actin polymerization

Thymosin beta10 is a small conserved acidic protein involved in the inhibition of actin polymerization. Studies have demonstrated that thymosin beta10 expression is regulated by extracellular signals that stimulate growth of thyroid cells both in vitro and in vivo, and suggest a role for this protein in thyroid diseases characterized by proliferation of follicular cells (10366416). Other studies have demonstrated that thymosin beta-10 is overexpressed in rat thyroid transformed cell lines and in human thyroid carcinoma tissues and cell lines. This evidence suggests that thymosin beta-10 detection may be considered a potential tool for the diagnosis of several human neoplasias (10487837).

SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. The novel nucleic acids and polypeptides are referred to herein as NOVX, or NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, NOV8, NOV9, NOV10 and NOV11 nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "NOVX" nucleic acid or polypeptide sequences.

In one aspect, the invention provides an isolated NOVX nucleic acid molecule encoding a NOVX polypeptide that includes a nucleic acid sequence that has identity to the nucleic acids disclosed in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33. In some embodiments, the NOVX nucleic acid molecule will hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of a NOVX nucleic acid sequence. The invention also includes an isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof. For example, the nucleic acid can encode a polypeptide at least 80% identical to a polypeptide comprising the amino acid sequences of SEQ ID NOS:2, 4, 6,

8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34. The nucleic acid can be, for example, a genomic DNA fragment or a cDNA molecule that includes the nucleic acid sequence of any of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33.

Also included in the invention is an oligonucleotide, *e.g.*, an oligonucleotide which includes at least 6 contiguous nucleotides of a NOVX nucleic acid (*e.g.*, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33) or a complement of said oligonucleotide. Also included in the invention are substantially purified NOVX polypeptides (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34). In certain embodiments, the NOVX polypeptides include an amino acid sequence that is substantially identical to the amino acid sequence of a human NOVX polypeptide.

The invention also features antibodies that immunoselectively bind to NOVX polypeptides, or fragments, homologs, analogs or derivatives thereof.

In another aspect, the invention includes pharmaceutical compositions that include therapeutically- or prophylactically-effective amounts of a therapeutic and a pharmaceutically-acceptable carrier. The therapeutic can be, *e.g.*, a NOVX nucleic acid, a NOVX polypeptide, or an antibody specific for a NOVX polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically- or prophylactically-effective amount of this pharmaceutical composition.

In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes a NOVX nucleic acid, under conditions allowing for expression of the NOVX polypeptide encoded by the DNA. If desired, the NOVX polypeptide can then be recovered.

In another aspect, the invention includes a method of detecting the presence of a NOVX polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the NOVX polypeptide within the sample.

The invention also includes methods to identify specific cell or tissue types based on their expression of a NOVX.

Also included in the invention is a method of detecting the presence of a NOVX nucleic acid molecule in a sample by contacting the sample with a NOVX nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to a NOVX nucleic acid molecule in the sample.

In a further aspect, the invention provides a method for modulating the activity of a NOVX polypeptide by contacting a cell sample that includes the NOVX polypeptide with a compound that binds to the NOVX polypeptide in an amount sufficient to modulate the activity of said polypeptide. The compound can be, *e.g.*, a small molecule, such as a nucleic acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon containing) or inorganic molecule, as further described herein.

Also within the scope of the invention is the use of a therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Von Hippel-Lindau (VHL) syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity, diabetes, autoimmune disease, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, hypercalcemia, Lesch-Nyhan syndrome, developmental defects, cataract, spinal cord injury, Alzheimer's disease, muscular dystrophy, acoustic trauma, cancer, learning and memory defects, infertility, cardiomyopathies, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect, atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect, valve diseases, tuberous sclerosis, scleroderma, endometriosis, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, dementia, stroke, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neurodegeneration, Familial hypercholesterolemia, hyperlipoproteinemia II phenotype, tendinous xanthomas, corneal arcus, coronary artery disease, planar xanthomas, webbed digits, hypercholesterolemia, fertility, xanthomatosis, Hepatitis C infection, regulation, synthesis, transport, recycling, or turnover of LDL receptors, Cerebral arteriopathy with subcortical infarcts and leukoencephalopathy, Epiphyseal dysplasia, multiple 1, Ichthyosis, nonlamellar and nonerythrodermic, congenital, Leukemia, T-cell acute lymphoblastoid, Pseudoachondroplasia, SCID, autosomal recessive, T-negative/B-positive type, C3 deficiency, Diabetes mellitus, insulin-resistant, with acanthosis nigricans, Glutaricaciduria, type I, Hypothyroidism, congenital, Leprechaunism, Liposarcoma, Mucopolidosis IV, Persistent Mullerian duct syndrome, type I, Rabson-Mendenhall syndrome, Thyroid carcinoma, nonmedullary, with cell oxyphilia, Erythrocytosis, familial, Malaria, cerebral, susceptibility to, Bleeding disorder due to defective thromboxane A2 receptor, Cerebellar ataxia, Cayman type, Convulsions, familial febrile, 2, Cyclic hematopoiesis, Fucosyltransferase-6 deficiency, GAMT deficiency, Cirrhosis, Psoriasis, Actinic keratosis, Tuberous sclerosis, Acne, Hair growth, alopecia,

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pigmentation disorders, endocrine disorders, trauma, immunological disease, respiratory disease, gastro-intestinal diseases, reproductive health, neurological diseases, bone marrow transplantation, metabolic and endocrine diseases, allergy and inflammation, nephrological disorders, hematopoietic disorders, urinary system disorders, Atopy; Osteoporosis-
5 pseudoglioma syndrome; Smith-Lemli-Opitz syndrome, type I; Smith-Lemli-Opitz syndrome, type II; Xeroderma pigmentosum, group E, subtype 2; Asthma, atopic, susceptibility to; Diabetes mellitus, insulin-dependent, 4; Susceptibility to IDDM; Angioedema, hereditary; Paranglioma, familial nonchromaffin, 2; neuroprotection; Lambert-Eaton myasthenic syndrome, digestive system disorders, all or some of the protease/protease inhibitor deficiency
10 disorders, diabetes mellitus non-insulin dependent, Acyl-CoA dehydrogenase, deficiency of long chain, Brachydactyly, type A1, Carbamoylphosphate synthetase I deficiency, Cardiomyopathy dilated II, Cataract Coppock-like, Cataract crystalline aculeiform, Cataract polymorphic congenital, Cataract variable zonular pulverulent, Cataracts punctate progressive juvenile-onset, Choreoathetosis familial paroxysmal, Craniofacial-deafness-hand syndrome,
15 Ichthyosis lamellar, type 2, Myopathy, desmin-related cardioskeletal, Resistance/susceptibility to TB, Rhabdomyosarcoma alveolar, Waardenburg syndrome type I and type III, Alport syndrome autosomal recessive, Bjornstad syndrome, Hematuria, familial benign, Hyperoxaluria primary, type 1, Syndactyly type 1, Hyperproglucagonemia, Bethlem myopathy, Brachydactyly type E, Brachydactyly-mental retardation syndrome, Finnish lethal
20 neonatal metabolic syndrome, susceptibility to 2, Simpson-Golabi-Behmel syndrome, type 1 and type 2, Beckwith-Wiedemann syndrome, pathogen infections, heart disease, prostate cancer, angiogenesis and wound healing, modulation of apoptosis, neuropsychiatric disorders, age-related disorders, pathological disorders involving spleen, thymus, lung, and peritoneal macrophages and/or other pathologies and disorders of the like.

25 The therapeutic can be, *e.g.*, a NOVX nucleic acid, a NOVX polypeptide, or a NOVX-specific antibody, or biologically-active derivatives or fragments thereof.

For example, the compositions of the present invention will have efficacy for treatment of patients suffering from the diseases and disorders disclosed above and/or other pathologies and disorders of the like. The polypeptides can be used as immunogens to produce antibodies
30 specific for the invention, and as vaccines. They can also be used to screen for potential agonist and antagonist compounds. For example, a cDNA encoding NOVX may be useful in gene therapy, and NOVX may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention will have efficacy for

treatment of patients suffering from the diseases and disorders disclosed above and/or other pathologies and disorders of the like.

The invention further includes a method for screening for a modulator of disorders or syndromes including, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like. The method includes contacting a test compound with a NOVX polypeptide and determining if the test compound binds to said NOVX polypeptide. Binding of the test compound to the NOVX polypeptide indicates the test compound is a modulator of activity, or of latency or predisposition to the aforementioned disorders or syndromes.

Also within the scope of the invention is a method for screening for a modulator of activity, or of latency or predisposition to disorders or syndromes including, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like by administering a test compound to a test animal at increased risk for the aforementioned disorders or syndromes. The test animal expresses a recombinant polypeptide encoded by a NOVX nucleic acid. Expression or activity of NOVX polypeptide is then measured in the test animal, as is expression or activity of the protein in a control animal which recombinantly-expresses NOVX polypeptide and is not at increased risk for the disorder or syndrome. Next, the expression of NOVX polypeptide in both the test animal and the control animal is compared. A change in the activity of NOVX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder or syndrome.

In yet another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a NOVX polypeptide, a NOVX nucleic acid, or both, in a subject (*e.g.*, a human subject). The method includes measuring the amount of the NOVX polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the NOVX polypeptide present in a control sample. An alteration in the level of the NOVX polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject. Preferably, the predisposition includes, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like. Also, the expression levels of the new polypeptides of the invention can be used in a method to screen for various cancers as well as to determine the stage of cancers.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with a disorder in a mammal by administering to the subject a NOVX polypeptide, a NOVX nucleic acid, or a NOVX-specific antibody to a subject (*e.g.*, a

human subject), in an amount sufficient to alleviate or prevent the pathological condition. In preferred embodiments, the disorder, includes, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like.

In yet another aspect, the invention can be used in a method to identify the cellular
5 receptors and downstream effectors of the invention by any one of a number of techniques commonly employed in the art. These include but are not limited to the two-hybrid system, affinity purification, co-precipitation with antibodies or other specific-interacting molecules.

NOVX nucleic acids and polypeptides are further useful in the generation of antibodies that bind immuno-specifically to the novel NOVX substances for use in therapeutic or
10 diagnostic methods. These NOVX antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. The disclosed NOVX proteins have multiple hydrophilic regions, each of which can be used as an immunogen. These NOVX proteins can be used in assay systems for functional analysis of various human disorders, which will help in understanding
15 of pathology of the disease and development of new drug targets for various disorders.

The NOVX nucleic acids and proteins identified here may be useful in potential
therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic,
20 diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration in vivo and in vitro of all tissues and cell types composing (but not limited to) those defined here.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention
25 belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods,
30 and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel nucleotides and polypeptides encoded thereby. Included in the invention are the novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to herein as "NOVX nucleic acids" or "NOVX polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table A provides a summary of the NOVX nucleic acids and their encoded polypeptides.

TABLE A. Sequences and Corresponding SEQ ID Numbers

NOVX Assignment	Internal Identification	SEQ ID NO (nucleic acid)	SEQ ID NO (polypeptide)	Homology
1	3352274	1	2	Calpain-like
2	21421174	3	4	Epsin-like
3	AC025263_da1	5	6	Low Density Lipoprotein B-like
4	AC026756_da1	7	8	Purinoreceptor
5a	sggc_draft_dj895c5_20000811_da1	9	10	CG8841-like
5b	CG54443-02	11	12	CG8841-like
6a	SC134912642_da1	13	14	Synaptotagmin-like
6b	CG56106-01	15	16	Synaptotagmin-like
7	wugc_draft_h_nh0781m21_20000809_da1	17	18	Serine Protease TLSP-like
8a	134913441_EXT	19	20	Glypican-2 Precursor-like
8b	CG50970-02	21	22	Glypican-2 Precursor-like
8c	CG50970-03	23	24	Glypican-2 Precursor-like
8d	CG50970-04	25	26	Glypican-2 Precursor-like
9	AC011005_da2/139943578	27	28	Mitogen-activated protein kinase kinase 2-like
10	sggc_draft_c333e1_20000804_da2	29	30	Zinc Finger Protein 276 C2H2-type
11a	GMAC079400_A	31	32	Thymosin beta 10-like
11b	CG109754-01	33	34	Thymosin beta 10-like

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

NOV1 is homologous to a Calpain-like family of proteins. Thus, the NOV1 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; Von Hippel-Lindau (VHL) syndrome, obesity, diabetes, autoimmune disease, systemic lupus

erythematosus, Lesch-Nyhan syndrome, developmental defects, Alzheimer's disease, muscular dystrophy, acoustic trauma, cancer, learning and memory defects, infertility and/or other pathologies/disorders.

NOV2 is homologous to a Espin-like family of proteins. Thus NOV2 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; cardiomyopathies, atherosclerosis, hypertension, congenital heart defects, obesity, infertility, cancer, autoimmune diseases, allergies, developmental defects, dementia, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, leukodystrophies, neurodegeneration and/or other pathologies/disorders.

NOV3 is homologous to a family of Low Density Lipoprotein B-like proteins. Thus, the NOV3 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example: Familial hypercholesterolemia, coronary artery disease, diabetes, atherosclerosis, Hepatitis C infection, Thyroid carcinoma, Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation, Psoriasis, Actinic keratosis, Tuberous sclerosis, Acne, Hair growth, alopecia, pigmentation disorders, endocrine disorders and/or other pathologies/disorders.

NOV4 is homologous to the Purinoceptor-like family of proteins. Thus, NOV4 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in various disease, pathologies and disorders.

NOV5 is homologous to the CG8841-like protein family. Thus NOV5 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example: cancer, trauma, immunological disease, respiratory disease, gastro-intestinal diseases, reproductive health, neurological and neurodegenerative diseases, bone marrow transplantation, metabolic and endocrine diseases, allergy and inflammation, nephrological disorders, hematopoietic disorders, urinary system disorders and/or other pathologies/disorders.

NOV6 is homologous to the Synaptotagmin-like family of proteins. Thus NOV6 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example: Atopy; Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-

Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection; metabolic disorders, Lambert-Eaton myasthenic syndrome and/or other pathologies/disorders.

NOV7 is homologous to members of the Serine Protease TLSP-like family of proteins.

- 5 Thus, the NOV7 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; cancer, neurological disorders, digestive system disorders, all or some of the protease/protease inhibitor deficiency disorders and/or other pathologies/disorders.

NOV8 is homologous to the Glypican-2 Precursor-like family of proteins. Thus,

- 10 NOV8 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; diabetes, diabetes mellitus non-insulin dependent, autoimmune disease, systemic lupus erythematosus, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ataxia-telangiectasia,
15 leukodystrophies, neurodegeneration, cancer, Cardiomyopathy, various cataract disorders Waardenburg syndrome type I and type III, Bjornstad syndrome, Simpson-Golabi-Behmel syndrome, type 1 and type 2, Beckwith-Wiedemann syndrome and/or other pathologies/disorders.

NOV9 is homologous to members of the Mitogen Activated Protein Kinase Kinase 2-

- 20 like family of proteins. Thus, the NOV9 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; atherosclerosis, metabolic diseases, pathogen infections, neurological diseases and/or other pathologies/disorders.

NOV10 is homologous to members of the Zinc Finger Protein 276 C2H2 type family

- 25 of proteins. Thus, the NOV10 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; cancer, trauma, immunological disease, respiratory disease, heart disease, gastro-intestinal diseases, reproductive health, neurological and neurodegenerative diseases, bone marrow transplantation, metabolic and endocrine diseases, allergy and inflammation,
30 nephrological disorders, hematopoietic disorders, urinary system disorders and/or other pathologies/disorders.

NOV11 is homologous to members of the Thymosin beta 10-like family of proteins.

Thus, the NOV11 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for

example; prostate cancer, immunological and autoimmune disorders (ie hyperthyroidism), angiogenesis and wound healing, modulation of apoptosis, neurodegenerative and neuropsychiatric disorders, age-related disorders, pathological disorders involving spleen, thymus, lung, and peritoneal macrophages and/or other pathologies/disorders.

The NOVX nucleic acids and polypeptides can also be used to screen for molecules, which inhibit or enhance NOVX activity or function. Specifically, the nucleic acids and polypeptides according to the invention may be used as targets for the identification of small molecules that modulate or inhibit, e.g., neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis.

Additional utilities for the NOVX nucleic acids and polypeptides according to the invention are disclosed herein.

NOV1

A disclosed NOV1 nucleic acid of 1947 nucleotides (also referred to as 3352274) encoding a novel Calpain-like protein is shown in Table 1A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TAG codon at nucleotides 1945-1947. The start and stop codons are in bold letters in Table 1A.

Table 1A. NOV1 Nucleotide Sequence (SEQ ID NO:1).

ATGGCATCCAGCAGTGGGAGGGTACCATCCAGCTCGTGGATGAGGAGGCTGGGGTCGGAGCCGGGCGCCTG
CAGCTTTTTCGGGGCCAGAGCTATGAGGCAATTCGGGCAGCCTGCCTGGATTTCGGGGATCCTGTTCCGCGAC
CCTTACTTCCCTGCTGGCCCTGATGCCCTTGGCTATGACCAGCTGGGGCCGGAATTCGAGAGAGGCCAAAGGC
GTGAAATGGATGAGGCCACAGGAGTTCTGTGCTGAGCCGAAGTTTCATCTGTGAAGACATGAGCCGCACAGAC
GTGTGTCAGGGGAGCCTGGGTAACGTGCTGGTTCCTGTCAGCTGCCGCTCCCTTACTCTGTATCCCCGGCTC
CTGCGCCGGGTGGTCCCTCCTGGACAGGATTTCCAGCATGGCTACGCAGGCGTCTTCCACTTCAGCTCTGG
CAGTTTGGCCGCTGGATGACGTCGTGGTGGATGACAGGCTGCCGTCGTGAGGGGAAGCTGATGTTTCGTG
CGCTCGAACACAGCGAATGAGTTCTGGGCCCCACTCCTGGAGAAGGCCACGCCAAGCTCCACGGCTCCTAT
GAGGTGATGCGGGCGGCCACATGAATGAGGCTTTTGTGGATTTACAGGCGGCGTGGGCGAGGTGCTCTAT
CTGAGACAAAACAGCATGGGGCTGTTCTCTGCCCTGCGCCATGCCCTGGCCAAGGAGTCCCTCGTGGGCGCC
ACTGCCCTGAGTGATCGGGGTGAGTACCGCACAGAAGAGGGCCTGGTAAAGGGACACGCGTATTCCATCACG
GGCACACACAAGGTAAGTCTGGGCTTACCAAGGTGCGGCTGCTGCGGCTGCGGAACCCATGGGGCTGCGTG
GAGTGGACGGGGCCTGGAGCGACAGCTGCCACGCTGGGACACACTCCCAACGAGTGCCGCGATGCCCTG
CTGGTGAAAAGGAGGATGGCGAGTTCTGGATGGAGCTGCGGGAATCCTCCTCCATTTGACACCGTGACG
ATCTGCTCGCTGAGCCCGAGGTGCTGGGCCCCAGCCCGAGGGGGCGGCTGGCACGTCCACACCTTCCAA
GGCCGCTGGGTGCGTGGCTTCAACTCCGGCGGGAGCCAGCCTAATGCTGAAACCTTCTGGACCAATCCTCAG
TTCCGTTTAACGCTGCTGGAGCCTGATGAGGAGGATGACGAGGATGAGGAAGGGCCCTGGGGGGCTGGGGG
GCTGCAGGGGCACGGGGCCAGCGCGGGGGGCGCACGCCAAGTGACGCTCCTTCTGTCCCTCATCCAG
CGCAACCGCGCGCCCTGAGAGCCAAGGGCCTCACTTACCTCACCGTTGGCTTCCACGTGTTCCAGGTGGAG
ATCGACGACGTGATCAGCGCAGACCTGCAGTCTCTCCAGGGCCCTACCTGCCCTGGAGCTGGGGTTGGAG
CAGCTGTTTCAGGAGCTGGCTGGAGAGGAGGAAGAATAATGCCTCTCAGCTCCAGGCCTTACTAAGCATT
GCCCTGGAGCCTGCCAGGGCCCATACCTCCACCCCCAGAGAGATCGGGCTCAGGACCTGTGAGCAGCTGCTG
CAGTGTTCGGGGGGCAAAGCCTGGCCTTACACCACTTCCAGCAGCTCTGGGGGTACCTCCTGGAGTGGCAG
GCCATATTTAACAAGTTTCGATGAGGACACCTCTGGAACCATGAACTCCTACGAGCTGAGGCTGGCACTGAAT
GCAGCAGTTTCCACCTGAACAACAGCTGACCCAGACCCTCACCAGCCGCTACCGGGATAGCCGCTGCGT
GTGGACTTCGAGCGGTTCTGTCTGTGTGGCCACCTCAGCTGCATCTTCCACTGCAGCCAGCACCTGGAT
GGGGGTGAGGGGTGATCTGCCTGACCCACAGACAGGTGAGCCAGGTGTGGATGGAGGTGGCCACCTTCTCC
TAG

The NOV1 nucleic acid sequence maps to chromosome 19 and has 430 of 631 bases (68%) identical to a *Gallus gallus* calcium protease mRNA (gb:GENBANK-ID:GGCPR0T|acc:X01415) ($E = 1.4e^{-90}$). Similarity information was assessed using public nucleotide databases including all GenBank databases and the GeneSeq patent database.

5 Chromosome information was assigned using OMIM and the electronic northern tool from Curatools to derive the the chromosomal mapping of the SeqCalling assemblies, Genomic clones, and/or EST sequences that were included in the invention.

In all BLAST alignments herein, the "E-value" or "Expect" value is a numeric indication of the probability that the aligned sequences could have achieved their similarity to the BLAST query sequence by chance alone, within the database that was searched. For example, the probability that the subject ("Sbjct") retrieved from the NOV1 BLAST analysis, e.g., *Gallus gallus* calcium protease mRNA, matched the Query NOV1 sequence purely by chance is $1.4e^{-90}$. The Expect value (E) is a parameter that describes the number of hits one can "expect" to see just by chance when searching a database of a particular size. It decreases exponentially with the Score (S) that is assigned to a match between two sequences. 15 Essentially, the E value describes the random background noise that exists for matches between sequences.

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, e.g.,

25 <http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/>. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNN") or the letter "X" in protein sequences (e.g., "XXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. Wootton and Federhen, Methods Enzymol 266:554-571, 1996.

30 The disclosed NOV1 polypeptide (SEQ ID NO:2) encoded by SEQ ID NO:1 has 648 amino acid residues and is presented in Table 1B using the one-letter amino acid code. Signal

P, Psort and/or Hydropathy results predict that NOV1 does not contain a signal peptide and is likely to be localized in the cytoplasm with a certainty of 0.7480.

Table 1B. Encoded NOV1 protein sequence (SEQ ID NO:2).

MASSSGRVTIQLVDEEAGVGAGRLQLFRGQSYEAIRAAACLDGILFRDPYFPAGPDALGYDQLGPDSEKAKG
VKWMPQEFCAEPKFICEDMSRTDVCQGSIGNCWFLAAAASLTLYPRLRRVVPFGQDFQHGYPVHFQQLW
QFGRWMDVVDDRLPVREGKLMFVRSEQRNEFWAPLLEKAYAKLHGSYEVMRGGHMNEAFVDFTGGEVLY
LRQNSMGLFSAIRHALAKESLVGATASDRGEYRTEEGLVKGHAYSITGTHKVS LGFTKVRLRLRNPGCV
EWTGAWSDCPRWDTLPTECRDALLVKKEDGEFWMELRDFLLHFDTVQICSLSPVGLGPSPEGGWVHTFQ
GRWVRGPNSSGQPNATFTWNTNQFRLTLLEPDEEDEDDEEGPWGGWGAAGARGPARGGRTPKCTVLLSLIQ
RNRRLRAKGLTYLTVGFHFVQVEIDDVISADLQSLQGPYLPLELGLQLFQELAGEEEELNASQLQALLSI
ALEPARAHTSTPREIGLRTCEQLLQCFGGQSLALHHFQQLWGYLLEWQAI FNKFD EDTSGTMNSYELRLALN
AAGFHLNNQLTQLTSRYRDSRLRVDFERFVSCVAHLTCIFHCSQHLDGGEVCLTHRQVSQVWMEVATFS

The NOV1 amino acid sequence has 405 of 456 amino acid residues (88%) identical to, and 429 of 456 amino acid residues (94%) similar to, a *Mus musculus* 720 amino acid residue protein (ptnr:TREMBLNEW-ACC:CAC10066) ($E = 4.1e^{-311}$).

NOV1 is expressed in at least the following tissues: Placenta, whole organism, kidney, liver, pancreas, small intestine. This information was derived by determining the tissue sources of the sequences that were included in the invention.

The disclosed NOV1 polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 1C.

Table 1C. BLAST results for NOV1

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 10303329 emb CAC10066.1 (AJ289241)	calpain 12 [Mus musculus]	720	404/456 (88%)	429/456 (93%)	0.0
gi 10303331 emb CAC10068.1 (AJ289241)	calpain 12 [Mus musculus]	462	404/456 (88%)	429/456 (93%)	0.0
gi 10303330 emb CAC10067.1 (AJ289241)	calpain 12 [Mus musculus]	502	404/456 (88%)	429/456 (93%)	0.0
gi 11230800 ref NP_068694.1	calpain 12 [Mus musculus]	449	300/342 (87%)	320/342 (92%)	1e-166
gi 5901916 ref NP_08989.1	calpain 11 [Homo sapiens]	702	274/706 (38%)	380/706 (53%)	1e-125

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 1D. In the ClustalW alignment of the NOV1 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and

can potentially be altered to a much broader extent without altering protein structure or function.

Table 1D. ClustalW Analysis of NOV1

1) Novel NOV1 (SEQ ID NO:2)

2) [gi|10303329|emb|CAC10066.1|](#) (AJ289241) calpain 12 [Mus musculus] (SEQ ID NO:35)

3) [gi|10303331|emb|CAC10068.1|](#) (AJ289241) calpain 12 [Mus musculus] (SEQ ID NO:36)

4) [gi|10303330|emb|CAC10067.1|](#) (AJ289241) calpain 12 [Mus musculus] (SEQ ID NO:37)

5) [gi|11230800|ref|NP_068694.1|](#) calpain 12 [Mus musculus] (SEQ ID NO:38)

6) [gi|5901916|ref|NP_008989.1|](#) calpain 11 [Homo sapiens] (SEQ ID NO:39)

NOV1	1	MASSSGRVTIQLVDEEAGVAGARLQLFRGQSYEAIRAACLDSGILFRDPYFPAGPDALGY	60
gi 10303329	1	MASGNRKVTIQLVDDGAGTGAGGPQLEKQNYEAIRRACLDSGILFRDPGFPAGPDALGY	60
gi 10303331	1	MASGNRKVTIQLVDDGAGTGAGGPQLEKQNYEAIRRACLDSGILFRDPGFPAGPDALGY	60
gi 10303330	1	MASGNRKVTIQLVDDGAGTGAGGPQLEKQNYEAIRRACLDSGILFRDPGFPAGPDALGY	60
gi 11230800	1	MASGNRKVTIQLVDDGAGTGAGGPQLEKQNYEAIRRACLDSGILFRDPGFPAGPDALGY	60
gi 5901916	1	MAAHIN--NSRLKAKGVGQHDN-AQNFQNSFEELRAACLRKGLFEDPLFPAEPSSLG	57
NOV1	61	DKLGPDSEKAGVBNMRPQEFCAEPKIFICEDMSRTDVCQGS LGNCWFLAAAASLTLYPRL	120
gi 10303329	61	DKLGPDSEKAGVBNMRPHEFCAEPKIFICEDMSRTDVCQGS LGNCWLLAAAASLTLYPRL	120
gi 10303331	61	DKLGPDSEKAGVBNMRPHEFCAEPKIFICEDMSRTDVCQGS LGNCWLLAAAASLTLYPRL	120
gi 10303330	61	DKLGPDSEKAGVBNMRPHEFCAEPKIFICEDMSRTDVCQGS LGNCWLLAAAASLTLYPRL	120
gi 11230800	61	DKLGPDSEKAGVBNMRPHEFCAEPKIFICEDMSRTDVCQGS LGNCWLLAAAASLTLYPRL	120
gi 5901916	58	KDLGPNSKNVQNI SWORPKDI INNPFIIMDGI SPTDI COGILGDCWLLAAIGSLITCPRL	117
NOV1	121	LYRVVPPGQGFQDGYAGVFHFQWLQFGRWVDVVDDRLPVREGKLMFVRSEQRNEFWAPL	180
gi 10303329	121	LYRVVPPGQGFQDGYAGVFHFQWLQFGRWVDVVDDRLPVREGKLMFVRSEQRNEFWAPL	180
gi 10303331	121	LYRVVPPGQGFQDGYAGVFHFQWLQFGRWVDVVDDRLPVREGKLMFVRSEQRNEFWAPL	180
gi 10303330	121	LYRVVPPGQGFQDGYAGVFHFQWLQFGRWVDVVDDRLPVREGKLMFVRSEQRNEFWAPL	180
gi 11230800	121	LYRVVPPGQGFQDGYAGVFHFQWLQFGRWVDVVDDRLPVREGKLMFVRSEQRNEFWAPL	180
gi 5901916	118	LYRVVPRGSGFKKNYAGIFHFQIHWQFCQWNVVVDDRLPTKNDKLVFVSESTERSEFWAL	177
NOV1	181	LEKAYAKLHGSYEVMRGCHMNEAFVDF TGGVGEVLYLRONSMGLFSALRHALAKESLVG	239
gi 10303329	181	LEKAYAKLHGSYEVMRGCHMNEAFVDF TGGVGEVLYLRONTPGVFAALRHALAKESLVG	239
gi 10303331	181	LEKAYAKLHGSYEVMRGCHMNEAFVDF TGGVGEVLYLRONTPGVFAALRHALAKESLVG	239
gi 10303330	181	LEKAYAKLHGSYEVMRGCHMNEAFVDF TGGVGEVLYLRONTPGVFAALRHALAKESLVG	239
gi 11230800	181	LEKAYAKLHGSYEVMRGCHMNEAFVDF TGGVGEVLYLRONTPGVFAALRHALAKESLVG	239
gi 5901916	178	LEKAYAKLSGSYEALSGCSTMGLEDF TGGVAQSFOLEPPQNLLRLRRAVERSSIMGC	237
NOV1	240	ATALSDRGETR--TDEGLVKGHAYSITGTHKMSLGFTKVRLRLRNPWGVEWTCAWSDS	297
gi 10303329	240	ATALSDRGETR--TDEGLVKGHAYSITGTHKMSLGFTKVRLRLRNPWGRVWESGVPWSDS	297
gi 10303331	240	ATALSDRGETR--TDEGLVKGHAYSITGTHKMSLGFTKVRLRLRNPWGRVWESGVPWSDS	297
gi 10303330	240	ATALSDRGETR--TDEGLVKGHAYSITGTHKMSLGFTKVRLRLRNPWGRVWESGVPWSDS	297
gi 11230800	240	ATALSDRGETR--TDEGLVKGHAYSITGTHKMSLGFTKVRLRLRNPWGRVWESGVPWSDS	297
gi 5901916	238	SIEVTSDSSEBSMTDKMLVRGHAYSITGLQDVHYRGKMETLIRVRNPWGRTEWNGAWSDS	297
NOV1	298	CPRWDTLPTEORDALLVKKEDGEFWMELQDFLTHFNTVQICSLSPFVLGPSPAGGGWHVH	357
gi 10303329	298	CPRWDTLPSEWRDALLVKKEDGEFWMELQDFLTHFNTVQICSLSPFVLGPSPAGGGWHVH	357
gi 10303331	298	CPRWDTLPSEWRDALLVKKEDGEFWMELQDFLTHFNTVQICSLSPFVLGPSPAGGGWHVH	357
gi 10303330	298	CPRWDTLPSEWRDALLVKKEDGEFWMELQDFLTHFNTVQICSLSPFVLGPSPAGGGWHVH	357
gi 11230800	298	CPRWDTLPSEWRDALLVKKEDGEFWMELQDFLTHFNTVQICSL-L-----PTP-----	344
gi 5901916	298	ARENEEVASDIQMQLLHNTEDGEFWMSTQDFLNNETLLEICMLTPDTLSGDYKS-YNHHT	356
NOV1	358	TFQGRWVRGPNSSGGSQPSAENFTWNPQFRLLTLEPDEE--DDEEGPWGGWGAAGARGPA	416
gi 10303329	358	IFQGRWVRGPNSSGGSQPSAENFTWNPQFRLLTLEPDEEEDDDDEEGPWGGWGAAGARGPA	417
gi 10303331	358	IFQGRWVRGPNSSGGSQPSAENFTWNPQFRLLTLEPDEEEDDDDEEGPWGGWGAAGARGPA	417
gi 10303330	358	IFQGRWVRGPNSSGGSQPSAENFTWNPQFRLLTLEPDEEEDDDDEEGPWGGWGAAGARGPA	417
gi 11230800	344	-----GWRRGGRLPDQPTVGGGYLLIGLKLREVTLLPDSLSQRW--WLCN-----EG	390
gi 5901916	357	FYEGSWRRGSSAGGCRNHPGTFTWNPQFKISLPEGDDPEDDAEGNVVVCTCLVALMQKNW	416
NOV1	417	RGGRTPKCTVLLSLIQNRNRRRLRAKGLTYLTVGFHFVQVEIDDDVIS---ADLQSLQGPY	472
gi 10303329	418	RGGRVPKCTVLLSLIQNRNRRCLRAKGLTYLTVGFHFVQIPEELLDLWDSRPRALLPGLL	477
gi 10303331	418	RGGRVPKCTVLLSLIQNRNRRCLRAKGLTYLTVGFHFVQIPEE-----GDR-----	462

gi 10303330	418	RGRVPKCTVLLSLIQNRRLRAKGLTYITVGPHVFQIPEEPRALAGT-AARRPL-GFL	475
gi 11230800	391	RPHKCWDYELEPSQTELP-----PFLKPLHVSPCLERG--T----TPTQALGWWA	435
gi 5901916	417	RHARQQGAQLQTIGFVLYAVPKFQNIQDVHLKKEFETKYQDHGFSEIFTNSREVSSQLR	476
NOV1	473	LP-----LELGLQLFQELAGEEEELN-ASQ-----	497
gi 10303329	478	RADRSVFCARRDVSRRCLPPGHYLVVPSASRVGDEADFTLRIFSERSHTAVEIDDDISA	537
gi 10303331	462	-----	462
gi 10303330	476	RPPR-----REPSLSPAAPWPLPGGTQRLARRR-----	502
gi 11230800	436	LP-----APWGMNRDAGRR-----	449
gi 5901916	477	LPP-----GEYIIIPSTFEPHRDADFLLRVFTEKHSESSELDEVN-----YAE	519
NOV1	497	----LQA-----LLSIALEPARAHTSTPREIGLRT	523
gi 10303329	538	DLDALQAPYKPLELELAQLFLELAGEEEELNALQLQTLISIALEPARANTRTPGEIGLRT	597
gi 10303331	462	-----	462
gi 10303330	502	-----	502
gi 11230800	449	-----	449
gi 5901916	520	QLQEEKVSEDDMDQDFLHLFKIVAGEGKEIGVYELQRLLRMAIKFKSFKTKGFGLDACR	579
NOV1	524	CEQLLQCFG-GQSLALHHFQQLWGYLEWQAIFNKFDDETSMTNSYELRLALNAAGFHL	582
gi 10303329	598	CEQLVQCFGRGQRLSLHHFQELWGHLMWQATFDKFDDETSMTNSCELRLALTAAGFHL	657
gi 10303331	462	-----	462
gi 10303330	502	-----	502
gi 11230800	449	-----	449
gi 5901916	580	CMINLMDKDGSGKLGLLEFKILWKKLKKWMDIFRECDQDHSGTLNSYEMRLVIEKAGIKL	639
NOV1	583	NNQLTQTLTSRYRDSRLRVDFERFVSCVAHLTCIF-HCSQHLDGGEGVICLTHRQVSQVW	641
gi 10303329	658	NNQLTQSLTSRYRDSRLRVDFERFVGCARLTICIFRHCCQHLDGGEGVVCLTH---KQW	713
gi 10303331	462	-----	462
gi 10303330	502	-----	502
gi 11230800	449	-----	449
gi 5901916	640	NNKVMQVLVARYADDDLIIDFDSFISCFRLKTMFTFFLTMDPKNTGHICLS----LEQW	695
NOV1	642	MEVATFS	648
gi 10303329	714	SEVATFS	720
gi 10303331	462	-----	462
gi 10303330	502	-----	502
gi 11230800	449	-----	449
gi 5901916	696	LQMTMWG	702

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro>). DOMAIN results for NOV1, as disclosed in Tables 1E and 1F, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Tables 1E, 1F and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (!) and “strong” semi-conserved residues are indicated by grey shading or by the sign (+). The “strong” group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.

Tables 1E and 1F lists the domain description from DOMAIN analysis results against NOV1. This indicates that the NOV1 sequence has properties similar to those of other proteins known to contain these domains.

Table 1E. Domain Analysis of NOV1

gnl|Pfam|pfam00648, Peptidase_C2, Calpain family cysteine protease.
(SEQ ID NO:89)
Length = 298 residues, 100.0% aligned
Score = 343 bits (881), Expect = 1e-95

NOV1	45	LFRDPYFPAGPDALGYDQLGPDSEKAKGVKWMRPQEFCAPKFCEDMSRTDVCQGS LGN	104
00648	1	LFVDPSFPAAPKSLGYKPLGP-----RGIEWKRPHEINENPQFIVGGATRTDICQ GALGD	55
NOV1	105	CWFLAAAASLTLYPRLRRVPPGQDFQHG YAGVFHFQLWQFGRWMDVVVDDRLPVREGK	164
00648	56	CWLLAALASLT LNEPLLRVPHDQSFQENYAGI FHF RFWQFGEWVDVVDDLLPTKD GK	115
NOV1	165	LMFVRSEQRNEFWAPLLEKAYAKLHGSYEV MRGGMNEAFVDF TGGVGEVLYLRQNS---	221
00648	116	LLFVHSAERNEFW SALLEKAYAKLNGCYEALSGGSTTEALEDLTGVCESYELKLAPSSM	175
NOV1	222	MGLFSALRHALAKESLVGA---TALSDRGEYRTEEGLVKGHAYSITGTHK VSLGFTKVRL	278
00648	176	LNLGNI IKMLERGSLLGCSIDITSPVDM EARMAGL VKGHAYSVTGVKEVNYRGE GVKL	235
NOV1	279	LRLRNPWGCVEWTGAWSDCPRWDTLPTECRDALLVKKEDGEFWME LRDFLLHFDTVQIC	338
00648	236	IRLRNPWGQVEWTGDWSDSPDWNIVDPDEKARLQLKFEDGEFWMSFEDFLRHFSRLEIC	295
NOV1	339	SLS 341	
00648	296	NLT 298	

Table 1F. Domain Analysis of NOV1

gnl|Smart|smart00230, CysPc, Calpain-like thiol protease family.;
Calpain-like thiol protease family (peptidase family C2). Calcium
activated neutral protease (large subunit). (SEQ ID NO:90)
Length = 323 residues, 99.1% aligned
Score = 342 bits (877), Expect = 4e-95

NOV1	27	FRGQSYEAI RAACLD SGILFRDPYFPAGPDALGYDQLGPDSEKAKGVKWMRPQEFCAPK	86
00230	1	FENQDYEE LRQECLEEGGLFVDPLFPAKPSSLFFSQLQRK-----FVWVKRPHEIFEDPP	55
NOV1	87	FICEDMSRTDVCQGS LGNCWFLAAAASLTLYPRLRRVPPGQDFQHG YAGVFHFQLWQF	146
00230	56	LIVGGASRTDICQGV LGDCWLLAALAALTREELLARVIPKDQEFSENYAGIYHFRFWRY	115
NOV1	147	GRWMDVVVDDRLPVREGKLMFVRSEQRNEFWAPLLEKAYAKLHGSYEV MRGGMNEAFVD	206
00230	116	GKWVDVVIDRLPTYNGDLLFMHSNSRNEFW SALLEKAYAKLRGCYEALKGGSTTEALED	175
NOV1	207	FTGGVGEVLYLRQNSMG---LFSALRHALAKESLVGATALSDRG---EYRTEEGLVKGHA	260
00230	176	LTGGVAESIELKKISKDPDELFDLKKAFERGS LMGCSIGAGTAVEEBEQKRNLGVKGHA	235
NOV1	261	YSITGTHK VSLGFTKVRLRLRNPWGCVEWTGAWSDCPRWDTLPTECRDAL-LVKKEDG	319
00230	236	YSVTDVREVDGR-RRQKLLRLRNPWGESEWNGPWSDDSP EWRSVSAEEKKNLGLTMDDDG	294

NOV1 320 EFWMELRDFLHFDTVQICSLSPEVL 345
 |||| ||| || |++| |
 00230 295 EFWMSFEDFLRHFTKVEICNLRPDWF 320

Cysteine protease activity is dependent on an active dyad of cysteine and histidine, the order and spacing of these residues varying in the 20 or so known families. Families C1, C2 and C10 are loosely termed papain-like, and nearly half of all cysteine proteases are found exclusively in viruses. Calpain is an intracellular protease involved in many important cellular functions that are regulated by calcium. The protein is a complex of 2 polypeptide chains (light and heavy), with three known forms in mammals: a highly calcium-sensitive (i.e., micro-molar range) form known as mu-calpain, mu-CANP or calpain I; a form sensitive to calcium in the milli-molar range, known as m-calpain, m-CANP or calpain II; and a third form, known as p94, which is found in skeletal muscle only. All three forms have identical light but different heavy chains. The heavy chain comprises four domains: domain 2 contains the catalytic region; domain 4 binds calcium and regulates activity. Domain 2 shows low levels of sequence similarity to papain; although the catalytic His has not been located by biochemical means, it is likely that calpain and papain are related. Domain 4 has four EF hand calcium-binding regions and is similar to sorcin and the Ca²⁺-binding region of calpain light chain. Calpain shows preferential cleavage for Tyr-with leucine or valine as the P2 residue.

Calpain is unique among the cysteine protease family of enzymes in that it combines thiol protease activity with calmodulin-like activity. The enzyme is implicated in a number of pathophysiological conditions (Donkor, *Curr Med Chem* 7(12):1171-1188, 2000). Proteases of the caspase and calpain families have been implicated in neurodegenerative processes, as their activation can be triggered by calcium influx and oxidative stress (Chan and Mattson, *J Neurosci Res* 58(1):167-90, 1999). Mitochondrial calpain plays an essential role in apoptotic commitment by cleaving Bax at its N-terminus and generating the Bax/p18 fragment, which in turn mediates cytochrome c release and initiates apoptotic execution (Gao and Dou, *J Cell Biochem* 80(1):53-72, 2001). Deficiency of the nCL-4 calpain protease has been implicated in neoplastic transformation (Liu et al., *J Biol Chem* 275(40):31093-8, 2000). Calpain proteases have been implicated in axon and myelin destruction following injury since they degrade structural proteins in the axon-myelin unit and may be responsible for destruction of myelinated axons adjacent to the lesion site following traumatic injury of the spinal cord (Shields et al., *J Neurosci Res* 61(2):146-50, 2000). Sperm calpain has been shown to be a novel component of the biochemical processes that regulate the fertilizing capacity of human spermatozoa (Rojas and Moretti-Rojas, *Int J Androl* 23(3):163-8, 2000). Findings have indicated that modulation of calpain activity contributes to muscular dystrophies by disrupting

normal regulatory mechanisms influenced by calpains (Tidball and Spencer, Int J Biochem Cell Biol 32(1):1-5, 2000).

The above defined information for NOV1 suggests that this calpain-like protein may function as a member of the calpain family. Therefore, the NOV1 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the NOV1 compositions of the present invention will have efficacy for treatment of patients suffering from Von Hippel-Lindau (VHL) syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity, diabetes, autoimmune disease, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, hypercalcemia, Lesch-Nyhan syndrome, developmental defects, cataract, spinal cord injury, Alzheimer's disease, muscular dystrophy, acoustic trauma, cancer, learning and memory defects and infertility. The NOV1 nucleic acid encoding calpain-like protein, and the calpain-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV2

A disclosed NOV2 nucleic acid of 1796 nucleotides (also referred to as 21421174) encoding a novel Epsin-like protein is shown in Table 2A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 40-42 and ending with a TAA codon at nucleotides 1771-1773. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 2A. The start and stop codons are in bold letters.

Table 2A. NOV2 nucleotide sequence (SEQ ID NO:3).

```
ATCGGGGCCCTGTGCCCTTGCTGCTGCAGCCGGGCACCATGTCGACCTCGTCCTTGAGGCGCCAGATGAAG
AACATCGTCCACAACACTACTCAGAGGCGGAGATCAAGGTTTCGAGAGGCCACGAGCAATGACCCCTGGGGCCCA
TCCAGCTCCCTCATGTGAGAGATTGCCGACCTCACCTACAACGTTGTGCGCTTCTCGGAGATCATGAGCATG
ATCTGGAAGCGGCTCAATGACCATGGCAAGAACTGGCGTCACGTTTACAAGGCCATGACGCTGATGGAGTAC
CTCATCAAGACCGGCTCGGAGCGCGTGTGCGAGCAGTGCAAGGAGAACATGTACGCCGTGCAGACGCTGAAG
GACTTCCAGTACGTGGACCGCGCAGGCAAGGACCAGGGCGTGAACGTGCGTGAGAAAGCTAAGCAGCTGGTG
GCCCTGCTGCGCGACGAGGACCGGCTGCGGGAAGAGCGGGCGCACGCGCTCAAGACCAAGGAAAAGCTGGCA
CAGACCGCCACGGCCTCATCAGCAGCTGTGGGCTCAGGCCCCCTCCCGAGGCGGAGCAGGCGTGGCCGAG
AGCAGCGGGGAGGAGGAGCTGCAGCTCCAGCTGGCCCTGGCCATGAGCAAGGAGGAGGCCGACAGCCCCCG
TCCTGCGGCCCCGAGGACGACGCCCAGCTCCAGCTGGCCCTTAGTTTGTAGCCGAGAAGAGCATGATAAGGAG
GAGCGGATCCGTGCGGGGATGACCTGCGGCTGCAGATGGCAATCGAGGAGAGCAAGAGGGAGACTGGGGGC
AAGGAGGAGTCGTCCCTCATGGACCTTGCTGACGTCTTACGGCCCCAGCTCCTGCCCCGACCAAGACCCC
TGGGGGGGCCACGACCCATGGCTGCTGCGTCCCCACGGCTGCCCCACCTCGGACCCCTGGGGCGGCCCC
CCTGTCCCTCAGCTGCTGATCCCTGGGGAGGTCCAGCCCCACGCGGCTCTGGGGACCCCTGGAGGCCT
GCTGCCCTGCAGGACCCCTCAGTTGACCCCTGGGGTGGGACCCAGCCCCCTGCAGCTGGGGAGGGGCCACG
CCTGATCCATGGGGAAGTTCCGATGGTGGTGGGGTCCCGGTGAGTGGGCCCTCAGCTCCGATCCCTGGACA
CCGGCCCCGGCCTTCTCAGATCCCTGGGAGGGTCACCTGCCAAGCCAGCACCAATGGCAAGGAGCCGGG
GGATTGACACGGAGCCCGACGAGTTTCTGACTTTGACCGACTCCGCACGGCACTGCCGCCCTCTCCCGG
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	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

5 A NOV2 polypeptide (SEQ ID NO:4) encoded by SEQ ID NO:3 has 577 amino acid residues and is presented using the one-letter code in Table 2B. Signal P, Psort and/or Hydropathy results predict that NOV2 does not contain a signal peptide and is likely to be localized to the mitochondrial matrix space with a certainty of 0.4600 and to the cytoplasm with a certainty of 0.4500.

MSTSSLRRQMKNIHVHNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVFSEIMSMIWKRLNDHGKNWR
 HVYKAMTLMLEYLIKTSERSVSQCKENMYAVQTLKDFQYVDRDGKQGVNVREKAKQLVALLRDEDRLREER
 AHALKTKKEKLAQTATASSAAVSGSGPPPEAEQAWQSSGGEELQLQLALAMSKEEADQPSCGPEDDAQLQLA
 LSLSREEHDKEERIRGGDDLRLQMAIEESKRETPGKEESSLLMDLADVFTAPAPAPTDPWGGPAPMAAAVPT
 AAPTSDPWGPGVPVPPAADPWGPGPATPASGDWPRAAGAPGSVDVWGGTPAPAPAGEPTDPDWGSSDGGVVP
 VSGPSASDPWTPAPAFSDPWGGSPAKPSTNGTAAGGFDTEPDEFSDFDRLRLTALPPLSRILPGELELLAGEV
 PARSPGAFDMSGVRGSLAEAVSGSPPAATPTPTPTPRKTPESFLGPNAALVDLDSLSVRGPPTPPGAKASNP
 FLPAGGAPATGPSVTNPFQAPATATLNLQRLRSPVPPVPGAPPTYISPLGGGPGPLPMMMPGPPAPNTNPFLL
 I.

15 mRNA (GENBANK-ID:CAB61412) ($E = 3.0e^{-313}$).

tissue because of the expression pattern of a closely related *Homo sapiens* EH domain-binding mitotic phosphoprotein (Epsin) mRNA (GENBANK-ID: gb:GENBANK-ID:AF073727|acc:AF073727).

NOV2 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 2C.

Table 2C. BLAST results for NOV2

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14758059 ref XP_034403.1	EH domain-binding mitotic phosphoprotein [Homo sapiens]	576	569/578 (98%)	569/578 (98%)	0.0
gi 3249559 gb AAC33823.1 (AF018261)	EH domain binding protein Epsin [Rattus norvegicus]	575	541/577 (93%)	548/577 (94%)	0.0
gi 7019369 ref NP_037465.1	EH domain-binding mitotic phosphoprotein [Homo sapiens]	551	544/578 (94%)	544/578 (94%)	0.0
gi 2072301 gb AAC60123.1 (U95102)	mitotic phosphoprotein 90 [Xenopus laevis]	609	356/613 (58%)	402/613 (65%)	1e-126
gi 3894395 gb AAC78608.1 (AF062084)	epsin 2a [Homo sapiens]	584	292/611 (47%)	348/611 (56%)	1e-102

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 2D.

Table 2D. ClustalW Analysis of NOV2

- 1) NOV2 (SEQ ID NO:4)
- 2) gi|14758059|ref|XP_034403.1| EH domain-binding mitotic phosphoprotein [Homo sapiens] (SEQ ID NO:40)
- 2) gi|3249559|gb|AAC33823.1| (AF018261) EH domain binding protein Epsin [Rattus norvegicus] (SEQ ID NO:41)
- 3) gi|7019369|ref|NP_037465.1| EH domain-binding mitotic phosphoprotein [Homo sapiens] (SEQ ID NO:42)
- 4) gi|2072301|gb|AAC60123.1| (U95102) mitotic phosphoprotein 90 [Xenopus laevis] (SEQ ID NO:43)
- 5) gi|3894395|gb|AAC78608.1| (AF062084) epsin 2a [Homo sapiens] (SEQ ID NO:44)

NOV2	1	MSTSSLRROMKNIHVNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVFSEIMSMI	60
gi 14758059	1	MSTSSLRROMKNIHVNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVFSEIMSMI	60
gi 3249559	1	MSTSSLRROMKNIHVNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVFSEIMSMI	60
gi 7019369	1	MSTSSLRROMKNIHVNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVFSEIMSMI	60
gi 2072301	1	-----MKNIHVNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVFSEIMSMI	51
gi 3894395	1	MTSSLRROMKNIHVNYSEAEIKVREATSNDPWGPSSSLMTEIADLTYNVVFSEIMSMV	60
NOV2	61	WKRLNDHGKNWRHVYKAMTLMLEYLIKTGSERVSQOCKENMYAVQTLKDFQYVDRDGDQ	120
gi 14758059	61	WKRLNDHGKNWRHVYKAMTLMLEYLIKTGSERVSQOCKENMYAVQTLKDFQYVDRDGDQ	120
gi 3249559	61	WKRLNDHGKNWRHVYKAMTLMLEYLIKTGSERVSQOCKENMYAVQTLKDFQYVDRDGDQ	120
gi 7019369	61	WKRLNDHGKNWRHVYKAMTLMLEYLIKTGSERVSQOCKENMYAVQTLKDFQYVDRDGDQ	120
gi 2072301	52	WKRLNDHGKNWRHVYKAMTLMLEYLIKTGSERVSQOCKENMYAVQTLKDFQYVDRDGDQ	111
gi 3894395	61	WKRLNDHGKNWRHVYKAMTLMLEYLIKTGSERVSQOCKENMYAVQTLKDFQYVDRDGDQ	120
NOV2	121	VNVREKAKQLVALLRDEDRLEERAHALKTKKLAQTAT---ASSAAGSGGP-----P	171
gi 14758059	121	VNVREKAKQLVALLRDEDRLEERAHALKTKKLAQTAT---ASSAAGSGGP-----P	171
gi 3249559	121	VNVREKAKQLVALLRDEDRLEERAHALKTKKLAQTAT---ASSAAGSGGP-----P	171
gi 7019369	121	VNVREKAKQLVALLRDEDRLEERAHALKTKKLAQTAT---ASSAAGSGGP-----P	171
gi 2072301	112	VNVREKAKQLVSLKDDERLEERAHALKTKKLAQTST---SSSASSTLNPA-----P	162
gi 3894395	121	VNVREKAKQLVALLRDEDRLEERAHALKTKKLAQTAT---ASSAAGSGGP-----P	171

NOV2 172 EAEQAWPOSSGEEELQLQLALAMSKEEADOPPPSCGP---EDDAQLQLALSLSRREEHDKKEE 228
gi|14758059| 172 EAEQAWPOSSGEEELQLQLALAMSKEEADOPPPSCGP---EDDAQLQLALSLSRREEHDKKEE 228
gi|3249559| 172 EAEQAWPOSSGEEELQLQLALAMSKEEADOPPPSCGP---EDDVQLQLALSLSRREEHDKKEE 228
gi|7019369| 172 EAEQAWPOSSGEEELQLQLALAMSKEEADOPPPSCGP---EEDVQLQLALSLSRREEHDKKEE 203
gi|2072301| 163 EGEQAWSSGEEELQLQLALAMSKEEABOVRAKPPPVSEELQLQLALSLSRREEHDKKEE 222
gi|3894395| 181 HSEQEQYKAGGSPASVYHGSTSPRVSSLEEQARPQTS---GEEELQLQLALAMSREVAEQEE 238

NOV2 229 RIRRGDDLRLQMAIEESKR---ETGGKEE-----SSLMDLADVFTAPAP-APTDPWG 277
gi|14758059| 229 RIRRGDDLRLQMAIEESKR---ETGGKEE-----SSLMDLADVFTAPAP-APTDPWG 277
gi|3249559| 229 RIRRGDDLRLQMAIEESKR---ETGGKEE-----SSLMDLADVFTTAPAP-PQASDPWG 277
gi|7019369| 204 RIRRGDDLRLQMAIEESKR---ETGGKEE-----SSLMDLADVFTTAPAP-APTDPWG 252
gi|2072301| 223 RIRRGDDLRLQMAIEESKR---GAPSKKEE-----QSSMDLADVFTTAPAPVAPTADPWG 274
gi|3894395| 239 RIRRGDDLRLQMAIEESKR---GAPSKKEE-----QSSMDLADVFTTAPAPVAPTADPWG 298

NOV2 278 GPAP-----MAAAVPTAAPTSDPWGGPPVPP- AADPWG-CPAPTASGDPWR-- 322
gi|14758059| 278 GPAP-----MAAAVPTAAPTSDPWGGPPVPP- AADPWG-CPAPTASGDPWR-- 322
gi|3249559| 278 GPAS-----VPTAVPVAAAASDPWGAAPVPP- AADPWG-CAAPTASGDPWR-- 322
gi|7019369| 253 GPAP-----MAAAVPTAAPTSDPWGGPPVPP- AADPWG-CPAPTASGDPWR-- 297
gi|2072301| 275 ASAAPPADPWAGGATPASVPAAPAAPDPWGGPPVATGSSSDPWGTCVQNTSTPGDPWGGT 334
gi|3894395| 299 PSAS-----TNQTNPWGGPAAPAS-TSDPWP-----S---FG-- 326

NOV2 322 ---PAAPAGPSVDPWGCTPAPAAAGEGPTP-DPWGSSDGGGVVPVSCPSASDPWTP-APAFS 377
gi|14758059| 322 ---PAAPAGPSVDPWGCTPAPAAAGEGPTP-DPWGSSDGGGVVPVSCPSASDPWTP-APAFS 376
gi|3249559| 322 ---PAAPTGPSVDPWGCTPAPAAAGEGPTP-DPWGSSDGGGVVPVSCPSASDPWTP-APAFS 376
gi|7019369| 297 ---PAAPAGPSVDPWGCTPAPAAAGEGPTP-DPWGSSDGGGVVPVSCPSASDPWTP-APAFS 351
gi|2072301| 335 QAVTSADVKSVDPPNPGGSGATTAIPS---DPWSSSP---VAQSVKKAADPWAPPAASFS 390
gi|3894395| 326 -----TKPAASIDPWGVPTGATQSVKPKNSDPWAASQQP-ASSACKRASAWGAVSTTKP 380

NOV2 378 DPWGGSPAKPSING-TAAGGFDTPEDEFSDFDLRLRTALP-PLSRILPGELELLAGEVPARS 436
gi|14758059| 377 DPWGGSPAKPSING-TAAGGFDTPEDEFSDFDLRLRTALP-TSGSSAGELELLAGEVPARS 435
gi|3249559| 377 DPWGGSPAKPSING-TAAGGFDTPEDEFSDFDLRLRTALP-TSGSSAGELELLAGEVPARS 434
gi|7019369| 352 DPWGGSPAKPSING-TAAGGFDTPEDEFSDFDLRLRTALP-TSGSSAGELELLAGEVPARS 410
gi|2072301| 391 DPWGGSPSKPNING-----TMGELDLLAGEVP-----MSRSLGSKS 426
gi|3894395| 381 VSVSGSFELESNLN-----G---TIKDDFSEFDNLRTSKKTAESVTS-----LPSQNNQNTTS 429

NOV2 437 PCAFDMSGVRGSLAEAVGSPPPAATPTPTPTPTRKTPESEFLGPNAALVDLDSLVSREGPPT 496
gi|14758059| 436 PCAFDMSGVRGSLAEAVGSPPPAATPTPTPTPTRKTPESEFLGPNAALVDLDSLVSREGPPT 495
gi|3249559| 435 PCAFDMSGVRGSLAEAVGSPPPAATPTPTPTPTRKTPESEFLGPNAALVDLDSLVSREGPPT 494
gi|7019369| 411 PCAFDMSGVRGSLAEAVGSPPPAATPTPTPTPTRKTPESEFLGPNAALVDLDSLVSREGPPT 470
gi|2072301| 427 PDAFDMSTMSGSLCDFSN-----PTRKTPESEFLGPNAALVDLDSLVSREGPPT 472
gi|3894395| 430 PDPFESQPLTVASSKPS-----ARKTPESEFLGPNAALVDLDSLVSREGPPT 473

NOV2 497 PCAKASNPFLPAGCPATGPSVTNPFQAPAPPATLTNLQRLSPV----- 539
gi|14758059| 496 PCAKASNPFLPAGCPATGPSVTNPFQAPAPPATLTNLQRLSPV----- 538
gi|3249559| 495 PCAKASNPFLPAGCPATGPSVTNPFQAPAPPATLTNLQRLSPV----- 537
gi|7019369| 471 PCAKASNPFLPAGCPATGPSVTNPFQAPAPPATLTNLQRLSPV----- 513
gi|2072301| 473 QNTKTSNPFLVCTGTPN---PTATNPFQAPAPPATLTNLQRLSPV----- 530
gi|3894395| 474 EXAQSLNPFLPAGCAPAN-SAPVNPFOVNPQPLTLNLQRLSPV----- 517

NOV2 539 -----PPVPCAPPTYISPLG-----GGPG-LPPMMPPG----- 566
gi|14758059| 538 -----PPVPCAPPTYISPLG-----GGPG-LPPMMPPG----- 565
gi|3249559| 537 -----PPVPCAPPTYISPLG-----GGPG-LPPMMPPG----- 564
gi|7019369| 513 -----PPVPCAPPTYISPLG-----GGPG-LPPMMPPG----- 540
gi|2072301| 531 PFASPMMSVSNMAPGIPPLANMAPVMGMQPMAGVPVGTLPACVPGMVLPPMMPPGQ---L 586
gi|3894395| 517 -----TSTSFQPCPGVESMAVASMTSAAQP-----ALCATGSSLTPLGPFAMNMVGS 565

NOV2 566 ---PPAPN-----TNPFL 577
gi|14758059| 565 ---PPAPN-----TNPFL 576
gi|3249559| 564 ---PPAPN-----TNPFL 575
gi|7019369| 540 ---PPAPN-----TNPFL 551
gi|2072301| 587 VAQPLLNLSTQAVTSTNPFL 609
gi|3894395| 566 VGIPPSAAQATG---TNPFL 584

Tables 2E and 2F list the domain description from DOMAIN analysis results against NOV2. This indicates that the NOV2 sequence has properties similar to those of other proteins known to contain these domains.

Table 2E Domain Analysis of NOV2

gnl|Pfam|pfam01417, ENTH, ENTH domain. The ENTH (Epsin N-terminal homology) domain is found in proteins involved in endocytosis and cytoskeletal machinery. The function of the ENTH domain is unknown. (SEQ ID NO:91)
Length = 123 residues, 92.7% aligned
Score = 173 bits (439), Expect = 2e-44

NOV2	17	YSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVAFSEIMSMIWKRLNDHGKNWRHVYK	76
		+ + + + + + +	
01417	1	YSELEKAVRKATNNDPWGPKGKHLDEILQGTIDEKSFPEIMDMLDKRLLE-GKNWRVVYK	59
NOV2	77	AMTLMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDQGVNVREKAKQLV	131
		+ + ++ + + ++ + + + +	
01417	60	ALILLHYLLRNGSERVVQEARRNRYIRELEDFRKVDSSGKDQGANIRTYAKYLL	114

5

Table 2F Domain Analysis of NOV2

gnl|Smart|smart00273, ENTH, Epsin N-terminal homology (ENTH) domain (SEQ ID NO:92)
Length = 127 residues, 89.8% aligned
Score = 149 bits (377), Expect = 3e-37

NOV2	18	SEAEIKVREATSNDPWGPSSSLMSEIADLTYNV-VAFSEIMSMIWKRLNDHGKNWRHVYK	76
		+ + + + + + + + +++ +	
01273	1	SDLEVKVRKATNNDWGPKGKHLREIIQGTTHNEKSSVAEIMAVLWRLNDT-KNWRVVYK	59
NOV2	77	AMTLMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDQGVNVREKAKQLV	131
		+ + ++ + + + + + +	
01273	60	ALILLHYLLRNGSPNVLEALRNRRNRLTSLDFRDIDSRGKDQGANIRTYAKYLL	114

The amino acid sequence of NOV2 also has high homology to other proteins as shown in Table 2G.

Table 2G. BLASTX results for NOV2

Sequences producing High-scoring Segment Pairs:				Reading High	Smallest		
				Frame	Score	P(N)	N
patp·AAB24234 Vesicle associated prot				13 - Homo sap, 576 aa... +1	3006	1.7e-312	1

Epsin (Eps15 interactor) is a cytosolic protein involved in clathrin-mediated endocytosis via its direct interactions with clathrin, the clathrin adaptor AP-2, and Eps15. The NH(2)-terminal portion of epsin contains a phylogenetically conserved module of unknown function, known as the ENTH domain (epsin NH(2)-terminal homology domain). Findings

suggest that epsin 1 may function in a signaling pathway connecting the endocytic machinery to the regulation of nuclear function (Hyman et al., J Cell Biol 149(3):537-46, 2000).

During endocytosis, clathrin and the clathrin adaptor protein AP-2, assisted by a variety of accessory factors, help to generate an invaginated bud at the cell membrane. One of these factors is Eps15, a clathrin-coat-associated protein that binds the alpha-adaptin subunit of AP-2. It has been proposed that epsin may participate, together with Eps15, in the molecular rearrangement of the clathrin coats that are required for coated-pit invagination and vesicle fission (Chen et al., Nature 394(6695):793-7, 1998).

It has been shown that both rat epsin and Eps15 are mitotic phosphoproteins and that their mitotic phosphorylation inhibits binding to the appendage domain of alpha-adaptin. Both epsin and Eps15, like other cytosolic components of the synaptic vesicle endocytic machinery, undergo constitutive phosphorylation and depolarization-dependent dephosphorylation in nerve terminals. Furthermore, their binding to AP-2 in brain extracts is enhanced by dephosphorylation. Epsin together with Eps15 is proposed to assist the clathrin coat in its dynamic rearrangements during the invagination/fission reactions. Their mitotic phosphorylation may be one of the mechanisms by which the invagination of clathrin-coated pits is blocked in mitosis and their stimulation-dependent dephosphorylation at synapses may contribute to the compensatory burst of endocytosis after a secretory stimulus (Chen et al., J Biol Chem 1999 Feb 5;274(6):3257-60).

The above defined information for NOV2 suggests that the NOV2 protein may function as a member of a family of novel Espin-like proteins. Therefore, the NOV2 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the NOV2 compositions of the present invention will have efficacy for treatment of patients suffering from cardiomyopathies, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect, atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect, valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation disorders, endometriosis, infertility, cancer, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, autoimmune diseases, allergies, immunodeficiencies, graft versus host disease, developmental defects, dementia, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, hypercalcemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neurodegeneration. The NOV2 nucleic acid encoding Espin-like proteins, and the Espin-like

proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV3

- 5 A disclosed NOV3 nucleic acid of 2973 nucleotides (also referred to as AC025263_da1) encoding a novel Low Density Lipoprotein B(LDLB)-like protein is shown in Table 3A. An open reading frame was identified beginning with a ATG initiation codon at nucleotides 1-3 and ending with a TAA codon at nucleotides 2971-2973. The start and stop codons are in bold letters in Table 3A.

Table 3A. NOV3 Nucleotide Sequence (SEQ ID NO:5)

ATGGCCACCGCGCAACCTCACCCGCGCTGAAGCGGCTGGATCTGCGCGACCCTGCGGCTCTTTTCGAGACG
CATGGAGCGGAGGAGATCCGCGGGCTGGAGCGCCAGGTTTCGGGCCGAGATCGAGCACAAGAAGGAGGAGCTG
CGGCAGATGGTGGGCGAACGGTACCGCGACCTGATCGAGGCGGCCGACCATCGGCCAGATGCGCCGCTGC
GCCGTGGGGCTAGTGGACGCGTGAAGGCCACCGACCAGTACTGCGCCCGCCTCCGCCAGGCCGGCTCGGCC
GCGCCCCGCGCCACCGCGGGCCAGCAGGTCACTCCCGTGCCCCACCCTGCGACCCGCGAGCGGGTCCCGG
AGCCCCCTGGCCTTGCAAGTCAACCCCGCCCCCTCTGTCACTCCAGACCCCGCGAGTCTCACCTTCCTTA
GCCAGGAGCCTATCCGCCCCCTCACCTTTGGGCTCTACCTGCTGTGTGCCACCTCCACAGCCTGCTCCAG
CTGGATTCTTCTAGTTCGCGATACAGTCCCGTCTCTCCCGGTTTCTTATACTCATCCGGCAGGTGGCAGCC
GCCAGCCACTTCCGGTCACTATTCTGCATGAAAGCAAGATGTTGCTCAAATGCCAAGGTGTGTCTGACCAA
GCTGTGGCCGAGGCCCTGTGCTCTATAATGCTCTTAGAAGAGAGTTCTCCTCGCCAAGCCCTCACAGACTTC
CTGCTGGCCAGAAAGGCACTATTCAAGAACTTCTCAACGACCCACCATGGTGTGGTATCAAGGCTCAG
ATTTGCTCATTAGTGGAGTTGCTGGCCACCCTCTGAAGCAAGCTCATGCCCTTTTCTACACTTTGCCAGAA
GGACTGTGCCAGATCCAGCCCTGCCATGTGGCTTGTCTTCTACTCTGGAGACCATCACAGGCCAGCAT
CTGCCGAAGGGCACTGGTGTCTGCGAGGAAGAGATGAACTCTGCAGCTGGTTTAAACACCTGCCAGCATCC
ATCGTCGAGTTCCAGCCAACTCCGAACCTTGCAATCCCATCAGTCAGGAATACCTGAAAGACACGCTG
CAGAAATGGATCCACATGTGTAATGAAGACATTAATAATGGGATCACCAACCTGCTCATGTACGTGAAGAGC
ATGAAGGTCTCGCGGGAATCCGGGACGCCATGTGGGAGTTACTTACCAATGAGTCCACCAATCACAGCTGG
GATGTGTATGTGCGCGGCTTCTGGAGAAGCCGCTCTGTTCTGGGAAGATATGATGCAGCAACTGTTCTCT
GACCGATTACAGACTCTGACAAAAGAGGCTTTGACTCCATCTCCAGTAGCTCCAAGGAGCTCTTGTTTCA
GCTTTGCAAGAACTTGAAAGCAGCACCCAGCAACTCCCTTCAAATAAGCACATCCACTTTGAGTACAAATG
TCGCTCTTCTCTGGTCTGAGAGTCTTAATGACCTGCCTTCCGATGCGGCCTGGGTGAGCGTGGCAAACCGG
GGTCAGTTAGGGGTGCTGCGCTCTCTATGAAAGCACAAGCCATCAGCCCTTGTGTACAGAACTTCTGTTCT
GCCCTGGATTCTAAGCTGAAGGTTAACTAGATGACCTCCTGGCTTACCTCCCTCTGATGACTCATCTG
CCCAAGGACGTTTCTCCACACAGGCCAAGAGTTCTGCCTTTGACAGATACGCAGATGCGGGGACCGTGCA
GAGATGCTGCGGACTCAGTCCGTGGCATGCATCAAGCACATCGTGGACTGCATCCGGGCAGAGCTACAGAGC
ATTGAAGAAGGTGTGCAAGGGCAACAGGATGCCCTCAACAGTGCCAAGCTGCACTCAGTTCTTTTCATGGCC
AGACTCTGCCTGTCCCTGGGAGAGCTGTGCCCCATCTGAAGCAGTGATCCTGGGAAAAATCAGAGAGCTCA
GAGAAACAGCAAGGGAGTTAGGGCTCTGAGAAAAAGGGAAAGGTGAAACTCAGGAAATCATTCCTACA
CAGGCCAAGTGGCAAGAGGTTAAAGAAGTACTCCTCCAGCAGAGCGTGTGGGCTACCAGGTCTGGAGCAGT
GCAGTTGTGAAAGTTTGTATTCATGGATTACCCAGTCATTACTTCTAGATGATGCTGGCTCAGTTCTGGCC
ACAGCCACCAGCTGGGATGAGCTAGAAATTCAGGAGGAGGCAGAGTCTGGCAGCAGTGTACATCCAAGATC
CGACTCCCTGCACAGCCGTCTGGTATGTACAGTCTTCTGTTTAGTTTATGCCAGGAAATTAATCGGGTT
GGAGGCCATGCCTTGCCAAAGGTGACATTACAGGAGATGCTGAAAAGCTGTATGGTTCAAGTAGTAGCTGCC
TATGAGAACTCTCCGAGAAAAACAGATTAAAGAAAGAGGTGCATTTCCAGTCACCCAGAACCGGGCGCTG
CAGCTGCTTATGATCTGCGTTACCTCAACATTGTTCTGACAGCCAAGGTGACGAGGTGAAGAGTGGCCGG
AGCAAGCCAGACTCCAGGATTGAGAAAGTACTGACCCTGGAAGCCCTCATTGATCCATTTGACCTGGAC
GTTTTACGCCACACCTCAACAGCAACCTTCATCGCCTGGTGACGCAACTTCTGTGCTGTTGGATTGGTG
ACTGGTACAGAAATCAGCTCGCCCCCGGAGCAGTACGTTCAACTCCCAAGAACCCATAACATCTGCCA
CTGGCATCCAGTCAGATCAGGAGGTTTGGACTTCTCCCACTGAGCATGACAAGCACTCGAAAGGCTAAATCA
ACCAAGAAATCAGAAACAAAGCTCAGGTTGGTCCCGGCACGCTCCACAGCTGGTGACCCGACAGTTCCT
GGCTCCTTGTTCAGACAGCTTGTCACTGAAGAAGACAAACGCTCTGCACCTTCATTATTCAAACCTGGCTGG
CTCTCTAGTATGACTAAGTAA

The disclosed NOV3 nucleic acid sequence maps to chromosome 19p13.1-13.3 and has 2360 of 2957 bases (79%) identical to a *Mus musculus* ldlBp (LDLB) mRNA (gb:GENBANK-ID:AF109377|acc:AF109377) (E = 0.0).

A disclosed NOV3 protein (SEQ ID NO:6) encoded by SEQ ID NO:5 has 990 amino acid residues, and is presented using the one-letter code in Table 3B. Signal P, Psort and/or Hydropathy results predict that NOV3 does not contain a signal peptide, and is likely to be localized to the nucleus with a certainty of 0.7600 and to the mitochondrial matrix space with a certainty of 0.4824.

Table 3B. Encoded NOV3 protein sequence (SEQ ID NO:6).

```
MATAATSPALKRLDLRDPALFETHGAEETRGLERQVRAEIEHKKEELRQMVGERYRDLIEAADTIGQMRRRC
AVGLVDVAVKATDQYCARLRQAGSAAAPRPPRAQQVSPRAPTLRPAGGSRSPWPCRSTPPPSVSPRPRESSPSL
ARSLSAPHPLGLYLLCCHLHSLQLDSSSSRYSPVLSRFPILIRQVAAASHFRSTILHESKMLLKQCGVSDQ
AVAEALCSIMLLEESSPRQALTDFLLARKATTQKLLNQPHHGAGIKAQICSLVELLATTLKQAHALFYTLPE
GLLPDPALPCGLLFSTLETTTGQHLPGKGTGLQEEMKLCWFKHLPASIVEFQPTLRTLAHPISQEYLDKTL
QKWIHMCNEDIKNGITNLLMYVKSMKGLAGIRDAMWELLTNESTNHSWDVLCRRLEKPLLFWEDMMQQLFL
DRLQTLTKEGFDSSSSSKELLVSALQELESSTSNPSNKHIFEYNMSLFLWSESPNDLPDAWVSVANR
GQLGVAGLSMKAQAISPCVQNFCSALDSKLVKLDLLAYLPSDDSSLPKDVSPPTQAKSSAFDRYADAGTVQ
EMLRTQSVACIKHIVDCIRAELOSIIEGVQGGQDALNSAKLHVSFLFMARLCLSLGELCPHLKQCILGKSESS
EKPAREFRALRKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFTQSLLLDDAGSVLA
TATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTLQEMLKSCMVQVVA
YEKLSEEKQIKKEGAFPVTONRALQLLYDLRYLNLVLTAKGDEVKSGRSKPDRIEKVTDHLEALIDPFDLD
VFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTFNSQEPHNILPLASSQIRRFGLPLSMTSTRKAKS
TRNIETKAQVGPPARSTAGDPTVPGSLFRQLVSEEDNTSAPSLFKLGLWSSMTK
```

The NOV3 amino acid sequence has 807 of 990 amino acid residues (81%) identical to, and 877 of 990 amino acid residues (88%) similar to, a *Mus musculus* 980 amino acid residue protein (ptnr:SPTREMBL-ACC:Q9Z160) (E = 0.0). The global sequence homology is 62.396% amino acid homology and 54.576% amino acid identity.

NOV3 is expressed in at least the following tissues based on literature sources: ovaries, liver, epidermis, fibroblast, blood leukocytes.

NOV3 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 3C.

Table 3C. BLAST results for NOV3

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14776518 ref XP_040307.1	hypothetical protein DKFZp762L1710 [Homo sapiens]	912	844/902 (93%)	853/902 (93%)	0.0
gi 15011849 ref NP_038609.2	low density lipoprotein B [Mus musculus]	980	799/994 (80%)	871/994 (87%)	0.0

gi 14776514 ref XP_040308.1	hypothetical protein DKFZp762L1710 [Homo sapiens]	666	660/667 (98%)	661/667 (98%)	0.0
gi 7243143 dbj BAA92619.1 (AB037802)	KIAA1381 protein [Homo sapiens]	961	892/951 (93%)	901/951 (93%)	0.0
gi 11360291 pir T50629	hypothetical protein DKFZp762L1710.1 [Homo sapiens]	438	436/439 (99%)	436/439 (99%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 3D.

Table 3D. ClustalW Analysis of NOV3

- 1) NOV3 (SEQ ID NO:6)
- 2) gi|14776518|ref|XP_040307.1| hypothetical protein DKFZp762L1710 [Homo sapiens] (SEQ ID NO:45)
- 2) gi|15011849|ref|NP_038609.2| low density lipoprotein B [Mus musculus] (SEQ ID NO:46)
- 3) gi|14776514|ref|XP_040308.1| hypothetical protein DKFZp762L1710 [Homo sapiens] (SEQ ID NO:47)
- 4) gi|7243143|dbj|BAA92619.1| (AB037802) KIAA1381 protein [Homo sapiens] (SEQ ID NO 48)
- 5) gi|11360291|pir|T50629 hypothetical protein DKFZp762L1710.1 [Homo sapiens] (SEQ ID NO:49)

NOV3	1	MATAATSPALKRLDLRDPALFETHGAEIIRGLERQVRAEIEHKKEELRMVGERYRDLI	60
gi 14776518	1	-----MVGERYRDLI	10
gi 15011849	1	MAAATASSALKRLDLRDPNALFETHGAEIIRGLERQVRAEIEHKKEELRMVGERYRDLI	60
gi 14776514	1	-----	1
gi 7243143	1	-ATAATSPALKRLDLRDPALFETHGAEIIRGLERQVRAEIEHKKEELRMVGERYRDLI	59
gi 11360291	1	-----	1
NOV3	61	EAADTIGOMRRCAVGLVDAVKATDQYCARLROAGSAAPRPPRAQQVSPRAPTLRPAGGSR	120
gi 14776518	11	EAADTIGOMRRCAVGLVDAVKATDQYCARLROAGSAAPRPPRAQQ-----PQQPSQ	61
gi 15011849	61	EAADTIGOMRRCAVGLVDAVKATDQYCARLROAGSAAPRPPRAQQ-----PQQPS	110
gi 14776514	1	-----	1
gi 7243143	60	EAADTIGOMRRCAVGLVDAVKATDQYCARLROAGSAAPRPPRAQQ-----PQQPSQ	110
gi 11360291	1	-----	1
NOV3	121	SPWPCRSTPPPSVSPRPRESSPSILARSLSAPHPLGLYLLCCHLSLLQLDSSSSRYSPVL	180
gi 14776518	62	EKFYSMAAQIKLLLEIPEKIWSMEAS-QCLHATQLYLLCCHLSLLQLDSSSSRYSPVL	120
gi 15011849	111	EKFYSMAAQIKLLLEIPEKIWSMEAS-QHLQATQLYLLCCHLSLLQLDSSSNRYSPVL	169
gi 14776514	1	-----	1
gi 7243143	111	EKFYSMAAQIKLLLEIPEKIWSMEAS-QCLHATQLYLLCCHLSLLQLDSSSSRYSPVL	169
gi 11360291	1	-----	1
NOV3	181	SRFPILIRQVAAASHFRSTILHESKMLLKCCGVSDQAVAEALCSIMLLEESSPRQALTD	240
gi 14776518	121	SRFPILIRQVAAASHFRSTILHESKMLLKCCGVSDQAVAEALCSIMLLEESSPRQALTD	180
gi 15011849	170	SRFPILIRQVAAASHFRSTILHESKMLLKCCGVSDQAVAEALCSIMLLEESSPRQALTD	229
gi 14776514	1	-----	1
gi 7243143	170	SRFPILIRQVAAASHFRSTILHESKMLLKCCGVSDQAVAEALCSIMLLEESSPRQALTD	229
gi 11360291	1	-----	1
NOV3	241	LLARKATICKLLNQPHHGAGIKAQICSLVELLATTLLQAHALFYTLPEGLLPDPALPCGL	300
gi 14776518	181	LLARKATICKLLNQPHHGAGIKAQICSLVELLATTLLQAHALFYTLPEGLLPDPALPCGL	240
gi 15011849	230	LLARKATICKLLNQPHHGAGIKAQICSLVELLATTLLQAHALFYTLPEGLLPDPALPCGL	289
gi 14776514	1	-----	1
gi 7243143	230	LLARKATICKLLNQPHHGAGIKAQICSLVELLATTLLQAHALFYTLPEGLLPDPALPCGL	289
gi 11360291	1	-----	1
NOV3	301	LFSTLETITCOHLP-KGTGVLQCEMKLCSWFKHLPASIVEFQPTLRTLHAHPISQEYLKDT	359
gi 14776518	241	LFSTLETITCOHPACKGTGVLQCEMKLCSWFKHLPASIVEFQPTLRTLHAHPISQEYLKDT	300
gi 15011849	290	LFSTLETITROHPTKGICALQCEMKLCSWLRHLPTSITFQPTLRTLHAHPISQEYLKDT	349

gi	14776514	1	-----MKLCSWFKHLPASIVEFQPTLRTLAHPISQEYLKDT	36
gi	7243143	290	LFSTLEITIGQHAGKGTGVLQDEMKLCSWFKHLPASIVEFQPTLRTLAHPISQEYLKDT	349
gi	11360291	1	-----	1
NOV3		360	LQKWIHMCNEDIKNGITNLLMYVKSMMKGLAGIRDAMWELLTNESTNHSWDVLCRRLEKP	419
gi	14776518	301	LQKWIHMCNEDIKNGITNLLMYVKSMMKGLAGIRDAMWELLTNESTNHSWDVLCRRLEKP	360
gi	15011849	350	LQKWIHMCNEDIKNGITNLLMYVKSMMKGLAGIRDAMWELLTNESTNHSWDVLCRRLEKP	409
gi	14776514	37	LQKWIHMCNEDIKNGITNLLMYVKSMMKGLAGIRDAMWELLTNESTNHSWDVLCRRLEKP	96
gi	7243143	350	LQKWIHMCNEDIKNGITNLLMYVKSMMKGLAGIRDAMWELLTNESTNHSWDVLCRRLEKP	409
gi	11360291	1	-----	1
NOV3		420	LLFWEDMMQQLFLDRLQTLTKEGFDSISSSSKELLVSALQELSESSTSNSPSNKHIHFEYN	479
gi	14776518	361	LLFWEDMMQQLFLDRLQTLTKEGFDSISSSSKELLVSALQELSESSTSNSPSNKHIHFEYN	420
gi	15011849	410	LLFWEDMMQQLFLDRLQTLTKEGFDSISSSSKELLVSALQELSESSTSNSPSNKHIHFEYN	467
gi	14776514	97	LLFWEDMMQQLFLDRLQTLTKEGFDSISSSSKELLVSALQELSESSTSNSPSNKHIHFEYN	156
gi	7243143	410	LLFWEDMMQQLFLDRLQTLTKEGFDSISSSSKELLVSALQELSESSTSNSPSNKHIHFEYN	469
gi	11360291	1	-----	1
NOV3		480	MSLFLWSESPNDLPSDAAWVSANRGQGLGVALSMKAQAISPCVQNFCSALDSKLVKVL	539
gi	14776518	421	MSLFLWSESPNDLPSDAAWVSANRGQGLGVALSMKAQAISPCVQNFCSALDSKLVKVL	480
gi	15011849	468	MSLFLWSESPNDLPSDAAWVSANRGQGLGVALSMKAQAISPCVQNFCSALDSKLVKVL	527
gi	14776514	157	MSLFLWSESPNDLPSDAAWVSANRGQGLGVALSMKAQAISPCVQNFCSALDSKLVKVL	216
gi	7243143	470	MSLFLWSESPNDLPSDAAWVSANRGQGLGVALSMKAQAISPCVQNFCSALDSKLVKVL	529
gi	11360291	1	-----	1
NOV3		540	DLAYLPSDDSSSLPKDVSP--QAKSSAFDRYADAGTVQEMLRQTSVACIKHIVDCIRAE	598
gi	14776518	481	DLAYLPSDDSSSLPKDVSP--QAKSSAFDRYADAGTVQEMLRQTSVACIKHIVDCIRAE	539
gi	15011849	528	DLAYLPSDDSSSLPKDVSP--QAKSSAFDRYADAGTVQEMLRQTSVACIKHIVDCIRAE	587
gi	14776514	217	DLAYLPSDDSSSLPKDVSP--QAKSSAFDRYADAGTVQEMLRQTSVACIKHIVDCIRAE	275
gi	7243143	530	DLAYLPSDDSSSLPKDVSP--QAKSSAFDRYADAGTVQEMLRQTSVACIKHIVDCIRAE	588
gi	11360291	1	-----LPKDVSP--QAKSSAFDRYADAGTVQEMLRQTSVACIKHIVDCIRAE	47
NOV3		599	QSIIEGVQGGQDALNSAKLHVSFLMARLQSLGELCPHLKQCILGKSESSEKPAREFRAL	658
gi	14776518	540	QSIIEGVQGGQDALNSAKLHVSFLMARLQSLGELCPHLKQCILGKSESSEKPAREFRAL	599
gi	15011849	588	QSIIEGVQGGQDALNSAKLHVSFLMARLQSLGELCPHLKQCILGKSESSEKPAREFRAL	647
gi	14776514	276	QSIIEGVQGGQDALNSAKLHVSFLMARLQSLGELCPHLKQCILGKSESSEKPAREFRAL	335
gi	7243143	589	QSIIEGVQGGQDALNSAKLHVSFLMARLQSLGELCPHLKQCILGKSESSEKPAREFRAL	648
gi	11360291	48	QSIIEGVQGGQDALNSAKLHVSFLMARLQSLGELCPHLKQCILGKSESSEKPAREFRAL	107
NOV3		659	RKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFQTSLLDDAGSV	718
gi	14776518	600	RKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFQTSLLDDAGSV	659
gi	15011849	648	RKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFQTSLLDDAGSV	707
gi	14776514	336	RKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFQTSLLDDAGSV	395
gi	7243143	649	RKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFQTSLLDDAGSV	708
gi	11360291	108	RKQGVKTQEIIPQAKWQEVKEVLLQQSVMGYQVWSSAVVKVLIHGFQTSLLDDAGSV	167
NOV3		719	LATATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTL	778
gi	14776518	660	LATATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTL	719
gi	15011849	708	LATATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTL	767
gi	14776514	396	LATATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTL	455
gi	7243143	709	LATATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTL	768
gi	11360291	168	LATATSWDELEIQEEAESGSSVTSKIRLPAQPSWYVQSFLFSLCQEIINRVGGHALPKVTL	227
NOV3		779	QEMLKSCMVQVVAAYEKLSEEKQIKKEGAFPVTQNRALQLLYDLRYLNIIVLTAKGDEVKS	838
gi	14776518	720	QEMLKSCMVQVVAAYEKLSEEKQIKKEGAFPVTQNRALQLLYDLRYLNIIVLTAKGDEVKS	779
gi	15011849	768	QEMLKSCMVQVVAAYEKLSEEKQIKKEGAFPVTQNRALQLLYDLRYLNIIVLTAKGDEVKS	827
gi	14776514	456	QEMLKSCMVQVVAAYEKLSEEKQIKKEGAFPVTQNRALQLLYDLRYLNIIVLTAKGDEVKS	515
gi	7243143	769	QEMLKSCMVQVVAAYEKLSEEKQIKKEGAFPVTQNRALQLLYDLRYLNIIVLTAKGDEVKS	828
gi	11360291	228	QEMLKSCMVQVVAAYEKLSEEKQIKKEGAFPVTQNRALQLLYDLRYLNIIVLTAKGDEVKS	287
NOV3		839	GRSKPDSRIEKVTDHLEALIDPFDLVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPR	898
gi	14776518	780	GRSKPDSRIEKVTDHLEALIDPFDLVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPR	839
gi	15011849	828	GRSKPDSRIEKVTDHLEALIDPFDLVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPR	887
gi	14776514	516	GRSKPDSRIEKVTDHLEALIDPFDLVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPR	575
gi	7243143	829	GRSKPDSRIEKVTDHLEALIDPFDLVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPR	888
gi	11360291	288	GRSKPDSRIEKVTDHLEALIDPFDLVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPR	347
NOV3		899	SSTFNSQEPHNILPLASSQIRFGLLPLSMTSTRKAKST--RNIETKAQVGPPARSTAGDP	957

nucleic acids and proteins of the invention are useful in potential therapeutic and diagnostic applications. For example, a cDNA encoding the NOV3 protein may be useful in gene therapy, and the NOV3 protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Familial hypercholesterolemia, hyperlipoproteinemia II phenotype, tendinous xanthomas, corneal arcus, coronary artery disease, planar xanthomas, webbed digits, hypercholesterolemia, fertility, coronary artery disease, diabetes, atherosclerosis, xanthomatosis, Hepatitis C infection, regulation, synthesis, transport, recycling, or turnover of LDL receptors, Cerebral arteriopathy with subcortical infarcts and leukoencephalopathy, Epiphyseal dysplasia, multiple 1, Ichthyosis, nonlamellar and nonerythrodermic, congenital, Leukemia, T-cell acute lymphoblastoid, Pseudoachondroplasia, SCID, autosomal recessive, T-negative/B-positive type, C3 deficiency, Diabetes mellitus, insulin-resistant, with acanthosis nigricans, Glutaricaciduria, type I, Hypothyroidism, congenital, Leprechaunism, Liposarcoma, Mucopolidosis IV, Persistent Mullerian duct syndrome, type I, Rabson-Mendenhall syndrome, Thyroid carcinoma, nonmedullary, with cell oxyphilia, Erythrocytosis, familial, Malaria, cerebral, susceptibility to, Bleeding disorder due to defective thromboxane A2 receptor, Cerebellar ataxia, Cayman type, Convulsions, familial febrile, 2, Cyclic hematopoiesis, Fucosyltransferase-6 deficiency, GAMT deficiency, Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation, Psoriasis, Actinic keratosis, Tuberous sclerosis, Acne, Hair growth, alopecia, pigmentation disorders and endocrine disorders. The NOV3 nucleic acid encoding Low Density Lipoprotein B-like protein, and the Low Density Lipoprotein B-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV4

A disclosed NOV4 nucleic acid of 1851 nucleotides (designated CuraGen Acc. No. Aco26756_da1) encoding a novel Purinoceptor-like protein is shown in Table 4A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 347-349 and ending with a TGA codon at nucleotides 1358-1360. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4A, and the start and stop codons are in bold letters.

Table 4A. NOV4 Nucleotide Sequence (SEQ ID NO:7)

CTAGAATTCAGCGGCCGCTGAATTCTAGCAGGCACGCTGGGCGCATGTCCGCTCGCCGGGGCTGCCAGA
ATCTTGGAATCCCAATCCGTGAGGTTCTGGGTGTGCTGGCATCAGGACAGCGGTCCACGAACGGTGTGT
TACCCAAATATTGACATCCTGCAGCTAGCCTCAAACAATCACAGCTACTTTCCAATTCAGAGAAAAAAA
GGCTAAAATTGGTAATCCTGATGAAAAATCAACAAAATACACATGAAGAGACAGCACTGAGAGCGAGTTAC
TGCTCATTGATTATATTGCCAACTGAACTCTCTTGTCTTCTTGCAAGATGAAAGGAGACAACCATGA
ATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCGATTATGCAGCTGCTTTGGAAATTGCAC
TGATGAAAAACATCCCACTCAAGATGCCTACCTCCCTGTTATTTATGGCATTATCTCCTCGTGGGATTT
CCAGGCAATGCAGTAGTGATATCCACTTACATTTCAAATGAGACCTTGAAGAGCAGCACCATCATT
TGCTGAACCTGGCCTGCACAGATCTGCTGTATCTGACAGCCTCCCTTCTGATTCACTACTATGCCAG
TGGCGAAAATCGGATCTTTGGAGATTTGATGTGAAGTTATCCGCTTCAGCTTCCATTTCAACCTGTAT
AGCAGCATCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCAATGAGCTGCT
TTTCCATTACAAAACTCGATGTGCAGTTGTAGCCTGTCTGTGGTGTGGATCATTCACTGGTAGCTGT
CATTCCGATGACCTTCTTGATCACATCAACCAACAGGACCAACAGATCAGCCTGTCTCGACCTACCAGT
TCGGATGAACTCAATACTATTAAGTGTACAACCTAATTTGACTGCAACTACTTTCTGCCTCCCTTGG
TGATAGTGACACTTTGCTATACCACGATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCT
TAAGCAGAAAGCAGCAAGGCTAACCATTCTGCTACTCCTTGCAATTTACGTATGTTTTTACCCTTCCAT
ATCTTGAGGGTCATTGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATG
AAGCTTACATCGTTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATGTGGTGGT
CAGCGAACAATTTAGCAGGCTGTCTGCTCAACAGTGAGATGCAAGTAAGCGGGAACCTTGAGCAAGCA
AAGAAAATTAGTTACTCAAAACAACCTTGAATATTTCAATTTACTTAACCAAAAAACAATACTGTCTGAT
ACTTTACCTAGCATCCTAAGATGTTGAGGATGTCTCCCTCAATGGAACCTCTGGTAAATACTGTGTATTC
AAGTAATCATGTGCCAAAGCCAGGGCAGAGCTTCTAGTTCTTTGCAATCCCTTTATTGAGCTCCTCCACT
GGGGAGATATAAGAATGGGATGCATGTATATCAGCAAAGTATTAGACATAGTATTACAAGCTATTGGAA
CTCAGAGGCATCTTAGAGAACATCTGTCTCCACCACTTACTATATATACACGGAACCAATTTCTTACC
CTTGCCCTAGATTGCTCAGTAAATTTGTGCCAAGATAGGAGAAAACCAATCTTTCACTCATCATTTTCAT
GCTTCTCTGCACTCTGGGCCTATTTGTATTGAACCATTAGACAATTCAAACCACTACTGTATCTTTCTT
AATATTATTTTACATCTCAGAGCTCTAC

The nucleic acid sequence of NOV4 has 419 of 717 bases (58%) identical to a *Mus musculus* P2Y purinoceptor mRNA (gb:GENBANK-ID: MMU22829|acc:U22829) (E = 9.8e-¹⁹).

A NOV4 polypeptide (SEQ ID NO:8) encoded by SEQ ID NO:7 is 337 amino acid residues and is presented using the one letter code in Table 4B. Signal P, Psort and/or Hydropathy results predict that NOV4 does not contain a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.6000.

Table 4B. NOV4 protein sequence (SEQ ID NO:8)

MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPNAVVISYIFKMRPWKSTIIMLN
LACTDLLYLTLSPFLIHYYASGENWIFGDFMCKFIRFSFHNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTR
CAVVACAVVWIIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKWYNLILTATTFCLPLVIVTLCTYTTII
HTLTHGLQTDSCCLKQKARRLTILLLLAFYVCFPLFHILRVIRIESRLLSISCSIENQIHEAYIVSRPLAALNTF
GNLLLYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP

The NOV4 amino acid sequence has 112 of 306 amino acid residues (36%) identical to, and 179 of 306 residues (58%) positive with, a *Mus musculus* 373 amino acid residue P2Y1 Purinoceptor protein (ATP Receptor) (ptnr:SWISSPROT-ACC:P49650) (E = 9.4e-56).

NOV4 is expressed in at least the following tissues corresponding to the 20 original pooled cDNAs it was amplified from: adrenal gland, bone marrow, brain – amygdala, brain – cerebellum, brain – hippocampus, brain – substantia nigra, brain – thalamus, brain – whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma – Raji, mammary

gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea and uterus.

Possible small nucleotide polymorphisms (SNPs) found for GPCR4 are listed in Table 4C. Depth represents the number of clones covering the region of the SNP. The putative allele frequency (PAF) is the fraction of these clones containing the SNP. A dash, when shown, means that a base is not present. The sign ">" means "is changed to."

Table 4C: SNPs			
Consensus Position	Depth	Base Change	PAF
193	39	T > -	0.051
527	33	C > T	0.061
591	32	C > T	0.062
614	38	C > T	0.316
721	33	T > -	0.061
823	33	A > G	0.061
929	33	G > A	0.061
1073	33	A > -	0.061

NOV4 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 4D.

Table 4D. BLAST results for NOV4					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 6679193.ref NP_03279.8.1 	purinergic receptor P2Y, G-protein coupled 1; P2Y1 receptor [Mus musculus]	373	109/299 (36%)	176/299 (58%)	1e-51
gi 4505557.ref NP_002554.1 	purinergic receptor P2Y, G-protein coupled, 1 [Homo sapiens]	373	108/299 (36%)	176/299 (58%)	5e-51
gi 2829680.sp P79928 P2Y8_XENLA	P2Y PURINOCEPTOR 8 (P2Y8) [Xenopus laevis]	537	104/283 (36%)	161/283 (56%)	7e-51
gi 1352693.sp P49652 P2YR_MELGA	P2Y PURINOCEPTOR 1 (ATP receptor) (P2Y1) (purinergic receptor) (6H1 orphan receptor) [Meleagris gallopavo]	362	106/299 (35%)	174/299 (57%)	7e-51
gi 464327.sp P34996 P2YR_CHICK	P2Y PURINOCEPTOR 1 (ATP receptor) (P2Y1) (purinergic receptor) [Gallus gallus]	362	106/299 (35%)	174/299 (57%)	7e-51

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 4E.

Table 4E ClustalW Analysis of NOV4

- 1) NOV4 (SEQ ID NO:8)
- 2) [gi|6679193|ref|NP_032798.1](#); purinergic receptor P2Y, G-protein coupled 1; P2Y1 receptor [Mus musculus] (SEQ ID NO:50)
- 3) [gi|4505557|ref|NP_002554.1](#) purinergic receptor P2Y, G-protein coupled, 1 [Homo sapiens] (SEQ ID NO:51)
- 4) [gi|2829680|sp|P79928|P2Y8_XENLA](#) P2Y purinoceptor 8 (P2Y8) [Xenopus laevis] (SEQ ID NO:52)
- 5) [gi|1352693|sp|P49652|P2YR_MELGA](#) P2Y purinoceptor 1 (ATP receptor) (P2Y1) (purinergic receptor) (6H1 orphan receptor) [Meleagris gallopavo] (SEQ ID NO:53)
- 6) [gi|464327|sp|P34996|P2YR_CHICK](#) P2Y purinoceptor 1 (ATP receptor) (P2Y1) (purinergic receptor) [Gallus gallus] (SEQ ID NO:54)

NOV4	1	MNEPLDYLANASDFPDYAAAFG-----NCTDENIPLKMHYLEVVIYG	41
gi 6679193	1	MTBVPWS-VVVPNGTDAAFLAGLGSWGNSTVASTAAVSSSFQCALTKTGQFQFYFLPAVYI	59
gi 4505557	1	MTBVLWP-MVVPNGTDAAFLAGPGSSWGNSTVASTAAVSSSFQCALTKTGQFQFYFLPAVYI	59
gi 2829680	1	MTEDIMATSYPTFLTTPYLPKM-----LLMNLTDNTEICVFDEGKFLFLPVSYS	51
gi 1352693	1	MTBALIS-AALNGTOPELLAG-----G-----WAAGNASTKCSLTKTGQFQFYFLPAVYI	48
gi 464327	1	MTBALIS-AALNGTOPELLAG-----G-----WAAGNATTKCSLTKTGQFQFYFLPAVYI	48
NOV4	42	YIELVGFFGNVAVISTYIFKMRPWKSSSTIIMNLACTDLLYLTSLPFLIHYAASGENWIF	101
gi 6679193	60	LVFTIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYFYFNKTDWIF	119
gi 4505557	60	LVFTIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYFYFNKTDWIF	119
gi 2829680	52	AVFMVGLPLNIAAMNIFIAKMRPWNPPTIVYMFNLALSDILYVLSLPTLVVYYADKNWPF	111
gi 1352693	49	LVFTITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYFYFNKTDWIF	108
gi 464327	49	LVFTITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYFYFNKTDWIF	108
NOV4	102	GDPMCKFIKFSFHNLYSSILFLTCISIFRYCVIHPMSCFSIHKTRCAVACAVVWIIIS	161
gi 6679193	120	GDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKNALIVSVLWLIIV	179
gi 4505557	120	GDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKNALICISVLWLIIV	179
gi 2829680	112	GEVLCKLVRFLFYANLYSSILFLTCISVHRYRGVCHPITSLRRMNAKHAYVICALVWLSV	171
gi 1352693	109	GDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKNAYVYVSSLVWALV	168
gi 464327	109	GDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKNAYVYVSSLVWALV	168
NOV4	162	LVAVIPMTFLITSTN-RTNRSACLDTSSDELTNIKWNLILATTFCLELVIVTLCYTT	220
gi 6679193	180	VVAISPILFYSGTGVRNKNTITCYDTTSDNYLRSYFIYSMCTTVAMFCIPLVLILGCYGL	239
gi 4505557	180	VVAISPILFYSGTGVRNKNTITCYDTTSDNYLRSYFIYSMCTTVAMFCIPLVLILGCYGL	239
gi 2829680	172	TLCVLPNLEVTVSP-KVKNITICHDTTPEDFARYVEYSTAIMCLLFCIPLCLIIAGCYGL	230
gi 1352693	169	VAVIAPILFYSGTGVRNKNTITCYDTTADNYLRSYFIYSMCTTVAMFCIPIFIVILGCYGL	228
gi 464327	169	VAVIAPILFYSGTGVRNKNTITCYDTTADNYLRSYFIYSMCTTVAMFCIPIFIVILGCYGL	228
NOV4	221	IIHTLTHGLQDS-----CLKOKARRITILLALAFYVCFLPFFHILRVIRIESRL---LSI	272
gi 6679193	240	IVKALIIYNOLDNS-----PLRRKSIYLVIIIVLTVFAVSYPFFHVMKTMNLRARLDFQTP	294
gi 4505557	240	IVRALIYKOLDNS-----PLRRKSIYLVIIIVLTVFAVSYPFFHVMKTMNLRARLDFQTP	294
gi 2829680	231	MTRELMKPIYSGNQQTLPYSYKRSIKTIIIVMIAFAICFMPFHTITRTLYYYARL---LGI	287
gi 1352693	229	IVKALIIKOLDNS-----PLRRKSIYLVIIIVLTVFAVSYPFFHVMKTMNLRARLDFQTP	283
gi 464327	229	IVKALIIKOLDNS-----PLRRKSIYLVIIIVLTVFAVSYPFFHVMKTMNLRARLDFQTP	283
NOV4	273	SCSIENQIHEAVIVSRPLAALNTFGNLLLYVVVSDNFQQAVCSTVRCKVS-----	322
gi 6679193	295	MCFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKAS-----RR-----	345
gi 4505557	295	MCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKAS-----RR-----	345
gi 2829680	288	KCYALNVINVTYKVTRPLASANSCTDPILYFLANDRYRRRLIRTVRRSSVFNRRCMHTN	347
gi 1352693	284	MCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSS-----RR-----	334
gi 464327	284	MCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSS-----RR-----	334
NOV4	322	-----GNLEQ-----AKKISYS-----N-----	335
gi 6679193	345	-----SEANLOS-----KSEEMTLN-----IIS-----	363
gi 4505557	345	-----SEANLOS-----KSEEMTLN-----IIP-----	363
gi 2829680	348	HPQTEPHMTAGPLPVISAEEIPSNIGSMVRDENGEGSREHRVETDTEINOMNRRSTIK	407
gi 1352693	334	-----SEPNVQS-----KSEEMTLN-----IIT-----	352
gi 464327	334	-----SEPNVQS-----KSEEMTLN-----IIT-----	352

NOV4	335	-----NP-----	337
gi 6679193	363	-----EFKQN---GDTSL-----	373
gi 4505557	363	-----EFKQN---GDTSL-----	373
gi 2829680	408	RNSTDKNDMKENRHGENYLPYVEVVEKEDYETKRENKKTTEQSSKTNAEQDELQTQIDSR	467
gi 1352693	352	-----EYKQN---GDTSL-----	362
gi 464327	352	-----EYKQN---GDTSL-----	362
NOV4	337	-----	337
gi 6679193	373	-----	373
gi 4505557	373	-----	373
gi 2829680	468	LKRGKWQLSSKKGAAQENEGHMEPSFEGETSTWNLLTPKMYGKKDRLAKNVEEVGYGK	527
gi 1352693	362	-----	362
gi 464327	362	-----	362
NOV4	337	-----	337
gi 6679193	373	-----	373
gi 4505557	373	-----	373
gi 2829680	528	EKELQNFPKA	537
gi 1352693	362	-----	362
gi 464327	362	-----	362

Table 4F lists the domain description from DOMAIN analysis results against NOV4.

5 This indicates that the NOV4 sequence has properties similar to those of other proteins known to contain these domains.

Table 4F. Domain Analysis of NOV4
gnl|Pfam|pfam00001, 7tm_1, 7 transmembrane receptor (rhodopsin family). (SEQ ID NO:93)
Length = 254 residues, 100.0% aligned
Score = 125 bits (315), Expect = 3e-30

NOV4	50	GNNAVISTYIFKMRPWKSSTIIMLNACTDLLYLTSPLFLIHHYASGENWIFGDFMCKFI	109
00001	1	GNLLVILVILRTRTKLRTPNIFLLNLAVADLLFLLTLPWALYYLVGGDWVFGDALCKLV	60
NOV4	110	RFSFHFNLVSSILFLTCSIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIIISLVAVIPMT	169
00001	61	GALFVVNGYASILLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVLALLLSLPPL	120
NOV4	170	FLITSTNRTNRSACLDLTSSDELNTIKWYNLILTATTFCPLVIVTLCYTTIIHTLTHGL	229
00001	121	LFSWLRVTEEGNTTVCLIDFPEESVKRSYVLLSTLVGFVLPLLVILVCYTRILRTLKRA	180
NOV4	230	QTDSLK-----QKARRLTILLLLAFYVCFPLPFHILRVIRIESRLLSISCSIQIHEA	283
00001	181	RSQRSCLKRRSSSERKAAKMLLVVVVVFVLCWLPYHIVLLDS-----LCLLSIWRVLP	235
NOV4	284	YIVSRPLAALNTFGNLLLY	302
00001	236	LLITLWLAYVNSCLNPIIY	254

10 The amino acid sequence of NOV4 has high homology to other proteins as shown in Table 4G.

Table 4G. BLASTX results for NOV4

					Smallest			
					Sum			
					Reading High	Prob		
Sequences producing High-scoring Segment Pairs:					Frame	Score	P(N)	
							N	
patp:AAU04584	Human	GPCR 3940,	Homo Sapiens	337 aa...	+2	1764	7.0e-181	1
patp:AAG80971	Human	nGPCR54 #2 -	Homo sapiens	337 aa...	+2	1601	1.3e-163	1

The above defined information for NOV4 suggests that this NOV4 protein may function as a member of a purinoceptor-like protein family. Therefore, the NOV4 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders. The NOV4 nucleic acid encoding purinoceptor-like protein, and the purinoceptor-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV5

NOV5 includes two novel CG8841-like proteins disclosed below. The disclosed proteins have been named NOV5a and NOV5b.

NOV5a

A disclosed NOV5a nucleic acid of 3146 nucleotides (also referred to as sggc_draft_dj895c5_20000811_da1) encoding a novel CG8841-like protein is shown in Table 5A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 2293-2295. A putative untranslated region downstream from the termination codon are underlined in Table 5A, and the start and stop codons are in bold letters.

Table 5A. NOV5a Nucleotide Sequence (SEQ ID NO:9)

ATGGGGTTCGACCGACTCCAAGCTGAACCTCCGGAAGCGCGGTGATCCAGCTCACCAACAAGACGCAGCCCGTGG
AAGCCACCGATGATGCTTTTGGGACCAGTTCTGGGCAGACACAGCCACCTCGGTGCAGGATGTGTTTGCACCT
GGTGCCGGCAGCAGAGATCCGGGCGGTGCGGAAGAGTCAACCTCCAACCTTGGCCACCTCTGTCTACAAGGCC
GTTGAGAAGCTGTGTGCAGGAGCTGAGAGTGCTGCCACTCGGAGAAGGAGAAGCAGATCTGCTCTGAATGCA
GCCGGCTGTCTACCCCGCGTGTCTGCCCTACATCTTTGAGGACCCCGACTGGAGGGGCTTCTCTGGTCCACAGT
GCCCCAGCAGGGAAGAGGATGATGAGCATGCCAGCCCTGGCCGAGTCTCTGCTCTGGCCATTGCTGAC
TGCTCTTCTGTGCCCGAAGCTTACCGTTTCAGGTCACCGCCACCGGAGGAGCACTGTGGACTCGGCAGAGGACGTCCACT
CCCTGGACAGCTGTGAATACATCTGGGAGGCTGGTGTGGGCTTCGCTCACTCCCCCAGCCCTAACTACATCCA
CGATATGAACCGGATGGAGCTGCTGAAACTGTGTGTCATGCTTCTCCGAGGCCATGTACTCTGCCCCAGCT
CCGGAAGTGGCAGCACCAACCCATGGGTTACGATTCTTTTGTCCACGGAGAAACAGACATGCCCTGCCCTCT
TCACCTCCCTCTCTCAACACCGTGTGTGCTCATGCCCTGTGGTTCAGGGATCCCCATAAACACCTGTCTCT
TCTGACTACGGGAACCCCTGGTGGAGGAGGCTGCCAGGTGCTCATTGTCACTTTGGACCACGACAGTGCC
AGCAGTGCCAGCCCCACTGTGGACGGCACCACTGGCACCGCCATGGATGATGCCGATGACTTCCAGTTCA
TCCTCAAGGGTATAGCCCGGCTGCTGTCCAACCCCTGCTCCAGACCTACTGTGCTTAACTCACCAAGAAGAT
CCAGTTCCACCAGGAGCTGCTAGTTCTCTTCTGGAAGCTCTGCGCACTTCAACAAGAAATCTCTCTCTTCGTG
CTGAAGAGCGAGCAGCTCCTAGACATCTTGTCCCCATCTCTCTCTCAACGATCCCGGGCCGATCAGT
CTCGGGTGGCCCTGATGCACATTTGTTCTTCACTTGTGCTCTGACGGGGGAGCGGAACCTTCGGGTGCG
GCTGAACAAACCTCTACTCAATCCGCGTGCCCATGGACATCCCACTCTTACAGGGACCCACGCCGACCTGCTC

ATTGTGGTGTTCACAGATCATCACCAGCGGGCACCAGCGGTTGCAGCCCCCTCTCGACTGCTGCTACCA
TCGTGGTCAACGTGTCCCCCTACCTCAAGAGCCTGTCCATGGTGACGCCAACAAGTTGCTGCACCTGCTGGA
GGCCTTCTCCACCACCTGGTTCCTTCTCTGCGCCGCCAGAACCCACCTGGTCTTCTTCTCTGAGGTC
TTCAACAAATCATCCAGTACCAGTTTATGGCACTCCAACTGGTCTACGCCATCATCCGCAAGCGCAGCA
TCTTCCACCAGCTGGCCAACCTGCCACCGACCCGCCACCATTCACAAGGCCCTGCAGCGGCGCGCGGAC
ACCTGAGCCCTTGTCTCGACCGGCTCCAGGAGGCACTCCATGGAGGGCTCCCGCCCGCTGCCCTGCA
GAGCCAGGCACCTCAAGACCACTTGGTGGCTACTCCAGGCATTGACAAGCTGACCGAGAAGTCCCAGGTGT
CAGAGGATGGCACCTTGGGTCCCTGGAACCTGAGCCCCAGCAGAGCTTGGAGGATGGCAGCCCGGTAAGGG
GGAGCCAGCCAGCATGGAGGGAGCAGCGCGCAGCGTCCACCTCATCAGCCAGTGGGCAGTGGAGCCCAACG
CCAGAGTGGGTCTCTCTGGAAGTCGAAGCTGCCGCTGCAGACCATCATGAGGCTGCTGCAGGTGCTGGTTC
CGCAGGTGGAGAAGATCTGCATCGACAAGGCCCTGACGGATGAGTCTGAGATCCTGCGGTTCTCTGCAGCATGG
CACCTTGGTGGGGTGTCTGCCCGTGCCCCACCCATCCTCATCCGCAAGTACCAGGCCAAGTCCGGGCACTGCC
ATGTGGTTCGCGACCTACATGTGGGGCGTCTATCTGAGGAATGTGGACCCCTGTCTGGTACGACACCG
ACGTGAAGCTGTTTGAGATACAGCGGGTGTGAGGATGAAGCCGACGAGGGGCTCAGTCTAGGGGAAGGCAGGG
CCTTGGTCCCTGAGGCTTCCCCATCCACATTCTGAGCTTAAATTACCAGATCAGGGCCTGGAACAGGCA
GAGTGGCCCTGAGTGTCTGAGCCCTAGAGACCCCTGTGGCCAGGACAATGTGAAGTGGCTCAGATCCCCCTCAA
CCCTAGGCTGGACTCACAGGAGCCCATCTCTGGGGCTATGCCCCACCCAGAGACCACTGCCCCCAACACTC
GGACTCCCTCTTTAAGACCTGGCTCAGTGTGGCCCTCAGTGCCACCCACTCCTGTGCTACCCAGCCCCAG
AGGCAGAGCCAAATGGGTCACTGTGCCCTAAGGGGTTTGACCAGGGAACACGGGCTGTCCCTTGGGTGC
CTGGACAGGGTAAGGGGGTGCTTCCAGCCTCCTAACCCAAAGCCAGCTGTTCCAGGCTCCAGGGGAAAAAGGT
GTGGCCAGGCTGCTCTCGAGGAGGCTGGGAGCTGGCCGATGCAAAAGCCAGACTGGGGCACCTCCCGTATC
CTTGGGGCATGGTGTGGGGTGGTGGGGTCTCTGCTATATTCTCTGGAATCCATGGAAATAGCCTGGCTCCC
TCTTACCCAGTAATGAGGGGAGGGAAGGAACTGGGAGGAGCCGTTTAGTCTCCCTGCCCTGCCACTGC
CTGGATGGGGCGATGCCACCCCTCATCCTTCAACCCAGCTCTGGCTCTGGGTCCCAACCCAGCCCCCGTG
TCAGAACATCTTGTCTGTGTAATCGGCCTCTTACAATAAAACCTCTGCTCCAAAAA

The NOV5a nucleic acid was identified on chromosome 17 and has 567 of 571 bases (99%) identical to a *Homo sapiens* DKFZp434I1120 mRNA (gb:GENBANK-ID:HSM802295|acc:AL137556) ($E = 1.1e^{-216}$)

- 5 A disclosed NOV5a polypeptide (SEQ ID NO:10) encoded by SEQ ID NO:9 is 764 amino acid residues and is presented using the one-letter code in Table 5B. Signal P, Psort and/or Hydropathy results predict that NOV5a contains a signal peptide and is likely to be localized in the plasma membrane with a certainty of 0.7300 and the microbody (peroxisome) with a certainty of 0.6075. The most likely cleavage site for a NOV5a peptide is between
- 10 amino acids 49 and 50, at: FAL-VP.

Table 5B. Encoded NOV5a protein sequence (SEQ ID NO:10)

MGSTDSKLNFRKAVIQLTKTPVEATDDAFWDQFWADTATSVQDVFALVPAEIRAVREESPSNLATLCYK
AVEKLVQGAESGCHSEKEKQIVLNCSSRLTRVLPYIFEDPDWRGFFWSTVPQQGEEDDEHARPLAESLLAI
ADLLFCPDFTVQSHRRSTVDSAEVDHSLDSEYIWEAGVGFAHSPQPNYIHDMMRMELLKLLTFCSEAMYL
PPAPESGSTNPWVQFFCSTENRHALLPLFTSLNLTVCAYDPVGYGIPYNHLLFSDYREPLVEEAAQVLIVTLD
HDSASSASPTVDGTTTGTAMDDADDQFILKGIARLLSNPLLQTYLPNSTKKIQPHQELLVLFWKLCDFNKK
FLFFVLKSSDVLDPILFVILFLNDARADQSRVGLMHIGVFILLLSGERNFVGRLNKPYSIRVPMIDIPVFTG
THADLLIVVFHKIITSQHRLQPLDFCLLTIVNVNSPYLKSLSMVTANKLLHLEAFSTTWLFSAQNHHLL
VFFLLEVENNNIIQYQFDGNSNLVYAIIRKRSIFHQLANLPTDPTIHKALQRRRTPEPLSRTGSQEGTSME
GSRPAAPAEPTLKTSLVATPGIDKLTEKSQVSEDTLRSLEPEPQSLLEDGSPAKGEPSQAWREQRRPSTS
SASQQWSPTEWVLSWKSPLQTIMRLQVLVPQVEKICIDKGLTDESEILRFLQHGTGLVGLLPVPHILIR
RKYQANSGTAMWFRITYMWGVIIYLRNVDPPVWYDTPVKLFETQVR

The NOV5a amino acid sequence has 397 of 638 amino acid residues (62%) identical to, and 478 of 638 amino acid residues (74%) similar to, a *Drosophila melanogaster* 837 amino acid residue CG8841 protein (ptnr:SPTREMBL-ACC:Q9V695) ($E = 5.9e^{-270}$).

- 15 NOV5a is expressed in at least the following tissues: adrenal gland/suprarenal gland,

amygdala, bone marrow, brain, colon, dermis, duodenum, hippocampus, hypothalamus, kidney, larynx, liver, lung, lymph node, lymphoid tissue, mammary gland/breast, ovary, pancreas, parotid salivary glands, pituitary gland, retina, small Intestine, spinal chord, stomach, substantia nigra, testis, thalamus, tonsils, umbilical vein, uterus, whole organism.

5 This information was derived by determining the tissue sources of the sequences that were included in the invention. In addition, the NOV5A is predicted to be expressed in testis tissue because of the expression pattern of a closely related *Homo sapiens* DKFZp434I1120 mRNA (gb:GENBANK-ID:HSM802295|acc:AL137556).

NOV5b

10 A disclosed NOV5b nucleic acid of 3314 nucleotides (also referred to as CG54443-02) encoding a novel CG8841-like protein is shown in Table 5C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 97-99 and ending with a TGA codon at nucleotides 2461-2463. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 5C, and
15 the start and stop codons are in bold letters.

Table 5C. NOV5b Nucleotide Sequence (SEQ ID NO:11)

GCGAGAGCCGCGGGGGCCGCGGAGCTGGAGCCGGAGCTGAAGCCGGAGCCGGGTGGAGTCTGGGCGGGG
GCCGGGCCGCGAGCGGGCTCCAGAGACATGGGGTCGACCGACTCCAAGCTGAACTTCGGAAGGCGGTGAT
CCAGCTCACCACCAAGACGCGAGCCCGTGAAGCCACCGATGATGCCCTTTGGGACCAGTTCTGGGCAGAC
ACAGCCACCTCGGTGCAGGATGTGTTGCACTGGTGCCGGCAGCAGAGATCCGGGCCGTGCGGGAAGAGT
CACCTCCAACCTTGGCCACCTGTGCTACAAGGCCGTTGAGAAGCTGGTGCAGGGAGCTGAGAGTGGCTG
CCACTCGGAGAGGAGAAGCAGATCGTCTGAACTGCAGCCGGCTGCTCACCCGCGTGTGCCCTACATC
TTTGAGGACCCGACTGGAGGGGCTTCTTCTGGTCCACAGTGCCCGGGGCAGGGCGAGGAGGGCAGGGAG
AAGAGGATGATGAGCATGCCAGGCCCTGGCCGAGTCCCTGCTCCTGGCCATTGCTGACCTGCTCTTCTG
CCCGGACTTCACGGTTCAGAGCCACCGGAGGAGCACTGTGGACTCGGCAGAGGACGTCCACTCCCTGGAC
AGCTGTGAATACATCTGGGAGGCTGGTGTGGGCTCGCTCACTCCCCCAGCCTAACTACATCCACGATA
TGAACCGGATGGAGCTGCTGAACTGCTGCTGACATGCTTCTCCGAGGCCATGTACCTGCCCCGAGCTCC
GGAAAGTGGCAGCACCAACCCATGGGTTCACTTCTTTGTTCCACGGAGAACAGACATGCCCTGCCCTC
TTCACTCCCTCCTCAACACCGTGTGTGCCATGACCCCTGTGGGCTACGGGATCCCCCTACAACCACTGCT
TCTTCTGACACCGGGGAACCCCTGGTGGAGGAGCTGCCAGGTGCTCATTGTCACTTTGGACCACGA
CAGTGCCAGCAGTGCCAGCCCCACTGTGGACGGCACCACCACTGGCACCGCCATGGATGATGCCGATCCT
CCAGGCCCTGAGAACCTGTTGTGAACTACCTGTCCCGCATCCATCGTGAGGAGGACTCCAGTTCATCC
TCAAGGGTATAGCCCGGCTGTGTCAACCCCTGCTCCAGACCTACCTGCCTAACTCCACCAAGAAGAT
CCAGTTCCACCAGGAGCTGCTAGTTCTTCTTCTGGAAGCTCTGCGACTTCAACAAGAAATTCCTCTTCTT
GTGCTGAAGAGCAGCGACGTCCTAGACATCCTTGTCCCCATCCTCTTCTTCTCAACGATGCCCGGGCCG
ATCAGTCTCGGGTGGGCTGATGCACATTGGTGTCTCATCTGTCTGCTTCTGAGCGGGAGCGGAACTT
CGGGGTGCGGCTGAACAAACCTACTCAATCCGCGTGCCCATGGACATCCAGTCTTTCACAGGGACCCAC
GCCGACCTGCTCATTGTGGTGTTCACCAAGATCATCACCAGCGGCACAGCGGTTGCAGCCCCCTTCTCG
ACTGCTGCTCACCATCGTGGTCAACGTGTCCCCCTACCTCAAGAGCCTGTCCATGGTGACCGCCAAACA
GTTGCTGCACCTGCTGGAGGCCTTCTCCACCCTGGTTCCTTCTTCTGCGCCCCAGAACCCACCTG
GTCTTCTTCTCCTGGAGGTCTTCAACAATCATCCAGTACCAGTTTGATGGCAACTCAACCTGGTCT
ACGCCATCATCCGCAAGCGCAGCATCTTCCACCAGCTGGCCAACTGCCACGGACCCGCCACCATTC
CAAGGCCCTGCAGCGCGCGCGGCAGACCTGAGCCCTTGTCTCGCACCGGCTCCAGGAGGGCACCTCC
ATGGAGGCTCCCGCCCCCTGCCCTGCAGAGCCAGGCACCTCAAGACCAGTCTGGTGGCTACTCCAG
GCATTGACAAGCTGACCGAGAAGTCCAGGTGTGAGAGGATGGCACCTTGCGGTCCCTGGAACCTGAGCC
CCAGCAGAGCTTGGAGGATGGCAGCCCGGTAAGGGGGAGCCAGCCAGGCATGGAGGGAGCAGCGCGCA
CCATCCACCTCATCAGCCAGTGGGCGTGGAGCCCAACGCCAGAGTGGGTCTCTCTGGAAGTCGAAGC
TGCCGCTGCAGACCATCATGAGGCTGCTGCAAGGTGCTGGTCCGCAAGTGGAGAAGATGTCATCGACAA
GGCCCTGACGGATGAGTCTGAGATCCTGCGGTTCTCTGCAGCATGGCACCCCTGGTGGGGCTGCTGCCCGTG
CCCCACCCATCCTCATCCGCAAGTACCAGGCCAATCGGGCACTGCCATGTGGTTCGACCTACATGT

Variable	Mean	SD	Min	Max
Age	34.2	10.5	18	65
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	2.1	9	16
Income	1.8	0.6	1	3
Occupation	1.5	0.5	1	3
Health status	1.2	0.4	1	2
Stress level	2.5	0.8	1	4
Life satisfaction	3.5	0.9	1	5
Resilience	4.2	1.1	1	6
Optimism	4.5	1.2	1	6
Self-efficacy	4.8	1.3	1	6
Emotional stability	5.2	1.4	1	6
Psychological well-being	5.5	1.5	1	6
Life meaning	5.8	1.6	1	6
Personal growth	6.0	1.7	1	6
Life goals	6.2	1.8	1	6
Life satisfaction	6.5	1.9	1	6
Life satisfaction	6.8	2.0	1	6
Life satisfaction	7.0	2.1	1	6
Life satisfaction	7.2	2.2	1	6
Life satisfaction	7.5	2.3	1	6
Life satisfaction	7.8	2.4	1	6
Life satisfaction	8.0	2.5	1	6
Life satisfaction	8.2	2.6	1	6
Life satisfaction	8.5	2.7	1	6
Life satisfaction	8.8	2.8	1	6
Life satisfaction	9.0	2.9	1	6
Life satisfaction	9.2	3.0	1	6
Life satisfaction	9.5	3.1	1	6
Life satisfaction	9.8	3.2	1	6
Life satisfaction	10.0	3.3	1	6
Life satisfaction	10.2	3.4	1	6
Life satisfaction	10.5	3.5	1	6
Life satisfaction	10.8	3.6	1	6
Life satisfaction	11.0	3.7	1	6
Life satisfaction	11.2	3.8	1	6
Life satisfaction	11.5	3.9	1	6
Life satisfaction	11.8	4.0	1	6
Life satisfaction	12.0	4.1	1	6
Life satisfaction	12.2	4.2	1	6
Life satisfaction	12.5	4.3	1	6
Life satisfaction	12.8	4.4	1	6
Life satisfaction	13.0	4.5	1	6
Life satisfaction	13.2	4.6	1	6
Life satisfaction	13.5	4.7	1	6
Life satisfaction	13.8	4.8	1	6
Life satisfaction	14.0	4.9	1	6
Life satisfaction	14.2	5.0	1	6
Life satisfaction	14.5	5.1	1	6
Life satisfaction	14.8	5.2	1	6
Life satisfaction	15.0	5.3	1	6
Life satisfaction	15.2	5.4	1	6
Life satisfaction	15.5	5.5	1	6
Life satisfaction	15.8	5.6	1	6
Life satisfaction	16.0	5.7	1	6
Life satisfaction	16.2	5.8	1	6
Life satisfaction	16.5	5.9	1	6
Life satisfaction	16.8	6.0	1	6
Life satisfaction	17.0	6.1	1	6
Life satisfaction	17.2	6.2	1	6
Life satisfaction	17.5	6.3	1	6
Life satisfaction	17.8	6.4	1	6
Life satisfaction	18.0	6.5	1	6
Life satisfaction	18.2	6.6	1	6
Life satisfaction	18.5	6.7	1	6
Life satisfaction	18.8	6.8	1	6
Life satisfaction	19.0	6.9	1	6
Life satisfaction	19.2	7.0	1	6
Life satisfaction	19.5	7.1	1	6
Life satisfaction	19.8	7.2	1	6
Life satisfaction	20.0	7.3	1	6
Life satisfaction	20.2	7.4	1	6
Life satisfaction	20.5	7.5	1	6
Life satisfaction	20.8	7.6	1	6
Life satisfaction	21.0	7.7	1	6
Life satisfaction	21.2	7.8	1	6
Life satisfaction	21.5	7.9	1	6
Life satisfaction	21.8	8.0	1	6
Life satisfaction	22.0	8.1	1	6
Life satisfaction	22.2	8.2	1	6
Life satisfaction	22.5	8.3	1	6
Life satisfaction	22.8	8.4	1	6
Life satisfaction	23.0	8.5	1	6
Life satisfaction	23.2	8.6		

5

10

MGSTDSKLNFRKAVIQLTTTKTPVEATDDAFWDQFWADTATSVDQVFALVPAAEIRAVREESPSNLATLCYKAVEK
LVQGAESGCHSEKEKQIVLNC SRLLTRVLPYIFEDPDWRGFFWSTVPGAGRGQGQEDDEHARPLAESLLLATADL
LFCPDTFTVQSHRRSTVDSAEDVHSLDSECEYIWEAGVGFAHSPQPNYIHMNRMELLKLLLTCTFSEAMYLPPAPESG
STNPWWQFFCSTENRHALPFTSLNLNTVCADYPGVGIPYNHLLFSDTGEPLVEEAAQVLIVTLDLHSDASSASPTV
DGTTTGAMDDADPPGPNELFVNYLSRIHREDFQILKGIARLLSNPLQLTVLPNSTKKIQFHQELLVFLWKLCD
FNKTKLFLVWLKSSVDLDILVPIILFLNDRADQSRVGLMHIGVFIILLLSGERNFGVRLNKPYSIRVPM DIPVFTG
THADLLIVVFHKIITS GHQRLQPLFDCLLTIVNVNVPYLKSLSMVTANKLLHLLLEAFSTTWFLFSAAQNHHLVFFL
LEVFNNI IQYQFDGNSNLVYAIIRKRSIFHQLANLPTDPPTIHKALQRRRRTPEPLSRTGSQEGTSMEGSRPAAPA
EPGTLKTSLVATPGIDKLTEKSQVSEDKTLRSLPEPEPQQSLEDGSPAKGEPSQAWREQRRPSTSSASGQWSPTPEW
VLWSKSKLPLOTIMRLLQVLVPOVEKICIDKGLTDESEILRFLDGLTVGLLPVHPHILIRKYQANS GTAMWFRTY
MWGVVIYLRNVDPVWYDTPVLKFEIORV

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carcinoma, uterine carcinoma, pancreatic adenocarcinoma, breast cancer. This information was derived by determining the tissue sources of the sequences that were included in the invention.

NOV5a and NOV5b are very closely homologous as is shown in the amino acid alignment in Table 5E.

Table 5E Amino Acid Alignment of NOV5a and NOV5b

	10	20	30	40
NOV5a	MGSTDSKLNFRKAVIQLT	TTKTPVEATDDAFWDQ	FWDQF	WADTA
NOV5b	MGSTDSKLNFRKAVIQLT	TTKTPVEATDDAFWDQ	FWDQF	WADTA
	50	60	70	80
NOV5a	TSVQDVFALVPAAEIRAV	REESPSNLATLCYKAVE	KLVQG	
NOV5b	TSVQDVFALVPAAEIRAV	REESPSNLATLCYKAVE	KLVQG	
	90	100	110	120
NOV5a	ABSGCHSEKEKQIVLNC	SRLLTRVLPYIFEDPD	WRGFFWS	
NOV5b	ABSGCHSEKEKQIVLNC	SRLLTRVLPYIFEDPD	WRGFFWS	
	130	140	150	160
NOV5a	TVP-----Q	QGEEDDEHARPLAESL	LLAIADLLFCPDFTV	
NOV5b	TVPGAGRCGQGEEDDEH	ARPLAESL	LLAIADLLFCPDFTV	
	170	180	190	200
NOV5a	QSHRRSTVDSAEDVHSL	DSCEYIWEAGVGFAHS	POPNYIH	
NOV5b	QSHRRSTVDSAEDVHSL	DSCEYIWEAGVGFAHS	POPNYIH	
	210	220	230	240
NOV5a	DMNRMELLKLLLT	CFSEAMYLPPAPESG	STNPWVQFFCST	
NOV5b	DMNRMELLKLLLT	CFSEAMYLPPAPESG	STNPWVQFFCST	
	250	260	270	280
NOV5a	ENRHALPLFTSL	LNTVCAYDPVGYGIPY	NHLLFS	SDYREPL
NOV5b	ENRHALPLFTSL	LNTVCAYDPVGYGIPY	NHLLFS	SDTGEPL
	290	300	310	320
NOV5a	VEEAAQVLIVTLDHDS	SASSASPTVDGTTTGT	AMDDAD---	
NOV5b	VEEAAQVLIVTLDHDS	SASSASPTVDGTTTGT	AMDDADPPG	
	330	340	350	360
NOV5a	-----D	FQFILKGIARLLSNP	LLQTYLPN	
NOV5b	PENL	FVNYLSRIHREEDFQ	FILKGIARLLSNP	LLQTYLPN
	370	380	390	400
NOV5a	STKKIQFHQELLV	FWKLCDFNKKFLFF	VLKSSDVLDILV	
NOV5b	STKKIQFHQELLV	FWKLCDFNKKFLFF	VLKSSDVLDILV	
	410	420	430	440
NOV5a	PILFFLNDARADQ	SRVGLMHIGVFILL	LLSGERNFGVRLN	
NOV5b	PILFFLNDARADQ	SRVGLMHIGVFILL	LLSGERNFGVRLN	
	450	460	470	480

gi 11360052 pir T46395	hypothetical protein DKFZp434I1120.1 (fragment) [Homo sapiens]	380	328/354 (92%)	328/354 (92%)	0.0
gi 7106107 emb CAB76033.1 (AL157917)	conserved hypothetical protein [Schizosaccharomyces pombe]	767	203/837 (24%)	360/837 (42%)	1e-44
gi 6648087 sp O13776.YE9G_SCHPO	hypothetical 104.8 KDA protein C17A5.16 IN CHROMOSOME I [Schizosaccharomyces pombe]	925	166/679 (24%)	299/679 (43%)	3e-31

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 5G.

Table 5G Clustal W Sequence Alignment

- 1) NOV5a (SEQ ID NO:10)
- 2) [gi|7303477|gb|AAF58533.1](#) (AE003822) CG8841 gene product [Drosophila melanogaster] (SEQ ID NO:55)
- 3) [gi|7505130|pir|T16522](#) hypothetical protein K02E10.2 [Caenorhabditis elegans] (SEQ ID NO:56)
- 4) [gi|11360052|pir|T46395](#) hypothetical protein DKFZp434I1120.1 (fragment) [Homo sapiens] (SEQ ID NO:57)
- 5) [gi|7106107|emb|CAB76033.1](#) (AL157917) conserved hypothetical protein [Schizosaccharomyces pombe] (SEQ ID NO:58)
- 6) [gi|6648087|sp|O13776.YE9G_SCHPO](#) hypothetical 104.8 KDA PROTEIN C17A5.16 IN CHROMOSOME I [Schizosaccharomyces pombe] (SEQ ID NO:59)

NOV5A	1	MCSTDSKLNFRKAVIQLTITKTPVEATDDAFWDQFWADTATSVQDVFAIVPAAEIRAVRE	60
gi 7303477	1	MCNTDSKLNFRKALVQLTQKNQKIDPSDEQFWQGHQTTLEDVFAIVTSSEIRQIRN	60
gi 7505130	1	MCAQGSRVDFKQVLDVTSKP---GKDDETFWDAQWNP--DSVNEIFAMISGEDIRKLRD	55
gi 11360052	1	MCSTDSKLNFRKAVIQLTITKTPVEATDDAFWDQFWADTATSVQDVFAIVPAAEIRAVRE	60
gi 7106107	1	MCSQOSKLDFFRNAILRLHEERN--IPKFDLTIWRLWTLPEETEDVFHLSIDDLTKVKD	57
gi 6648087	1	MCGQESKIAFORGIARLASQPD--IPLDDEVVSLWSVP-ESCPEVYDFPPGLIREMRD	57
NOV5A	61	ESPSNLATLCYKAVEKLVQGAESGCHSEKEKQ---IVLNC SRLLTRVLPYIFED---PDW	114
gi 7303477	61	ENPANLATLCYKAVEKLAQAVDSSCRTQAEQQ---CVLNCVRLLVRCIPYIFED---EKN	114
gi 7505130	56	ESPKNLATLVYKTVKELQFSRNHPATIDQK-----TINAIRLLTRIVPYLLED---AEW	107
gi 11360052	61	ESPSNLATLCYKAVEKLVQGAESGCHSEKEKQ---IVLNC SRLLTRVLPYIFED---PDW	114
gi 7106107	58	NAPENLQTI IAVLWDKLEDLQKETLFPDPAAPTTCALNCMRLLTRLMPIIFEDKSMLEW	117
gi 6648087	58	HAFVNLEKILLVLTSLRFLAKNDKKFPNPETAPASEALNCIRLLTRIIPFLNEKLDLEEW	117
NOV5A	115	RGFWSTVPEQG-----EEDDEHARPLAESLILA	143
gi 7303477	115	RDFWSSLES-----QD---KTMPLAQSLINA	138
gi 7505130	108	RGYFWSPIPHG-----DAAKPLAAVLLET	131
gi 11360052	115	RGFWSTVPEGAG-----RGG-GEEDDEHARPLAESLILA	147
gi 7106107	118	FDYFAWTVPKD-----PNINTERGASFLNT	142
gi 6648087	118	HQKFWWSLRKKRNLPKENSELDLSNFQDDLDFENSISQKNEFSQKSPSVLSPVSTFPAS	177
NOV5A	144	IADLLFCPDFTVQSHRRSTVDSAEDVHSLDS-----	174
gi 7303477	139	TCDLLFCPDFTVTATRRAGPEKAEELANIDS-----	169
gi 7505130	132	LSDLLFCPEFTIT---HANGKIDDLSTIDS-----	159
gi 11360052	148	IADLLFCPDFTVQSHRRSTVDSAEDVHSLDS-----	178
gi 7106107	143	VVDYLFELINFITIP---AHN---DLTHGVH-----	165
gi 6648087	178	SISTDASSDVSAADVSVGGSSTIKEIGSTIEETFTHEKTLMEELLDTVFRLLCRGFTLPL	237
NOV5A	174	-----CEYIWEAGVCFASHPOPN-YIHDMNRMEILLKLLLTCSFSEAMYLPPAPESGSTNP	227
gi 7303477	169	-----CEYIWEAGVCFASPPHN-AHMERRRTEILLKLLLTCSFSEPMYRSPQ-QSEEPNK	221
gi 7505130	159	-----CEYIWEAGVCSGNKPMV-ALHYQNRTEILLKLLLTCSFSEALIYAPVS--DETRLR	210

gi|11360052| 178 -----CEYIWEAGVGFHSPQPN-YIHDNRMLLKLLLCFSEAMYLPPAPESGSTNP 231
gi|7106107| 165 -----YCIWETGVVYHPTMLKE-RSYELHREVEVLRLLSLSEEIYRTDG---NGSSC 214
gi|6648087| 238 SSPEQYAYIIWENGIGTTTQEKTKELAFNRIEVLRLLLVLISKRLYRSSE---VASHT 294

NOV5A 228 WVQFFCSTENRHALLPLFTSLNLTVCAYDPVCGYGPYNHLL-ESLYREPLVEEAAQVLIIVT 286
gi|7303477| 222 WIAVFTSADNRHALLPLFTSELNLTVCSDYDPVCGYGPYNHLL-EDTTEPLVEACLQLLIIVT 280
gi|7505130| 211 WVIHFTSVTNPHVLPIFTSLNLTVCAYDPVCGYGPYNHLL-ENDSREPLVEIALQVLIIVC 269
gi|11360052| 232 WVQFFCSTENRHALLPLFTSLNLTVCAYDPVCGYGPYNHLL-ESLYREPLVEEAAQVLIIVT 290
gi|7106107| 215 CAYVASIANRRLVLQLLSSLLNTIAMRNTMFWKPEFLPLD-NSVAHMSLIEYCFSVLLIL 273
gi|6648087| 295 LTYLTCVANKQLILVFLYSLINTTLRLRPDSWKASVSTLVPNYSSIAVSKLTSQILLLF 354

NOV5A 287 LDHDSASSASPTVDGTTTGTAMDDAD-----DFQFILKGIARLLSN 327
gi|7303477| 281 LDHDMVVQQQLTQPGQASYDEGNCGD-----NLFINYLRSVRHREDDFHEVLKGIIRLLNN 335
gi|7505130| 270 LDKETQPNITDDS-----G-YKD-----NYFINYLRSRIHREEDDFDKLGIARLLSN 314
gi|11360052| 291 LDHDSASSASPTVDGTTTGTAMDDADPPGPNLEFVNYSRIHREEDDFQILKGIARLLSN 350
gi|7106107| 274 MSEENNGTPCYNNYRSS-KNTLPKN-----YFSILLKQLQPYSDFIILDGMSRLLYP 326
gi|6648087| 355 LDHTPHETTVEYFRQRLNLSPGAATEN-----QYRLVESRLQLQADYEFLVNELYRLINA 409

NOV5A 328 PLLQT--YLPNSTKKIQFHQELLVLPWKLCDPNKKLFFVLKSSDVLDILVPIILFFLND 385
gi|7303477| 336 PLVQN--YLPNSTKRLHCHQELLILPWKICDYNKKFLYFVLKSSDVLDILIPILYHLNYS 393
gi|7505130| 315 PHHSSSVLPNSTKRVNFHQLLVLLWKCCETNOKMFYVLKTSADVLDILVPIILYHISDA 374
gi|11360052| 351 LLLQK--KKKKKKKKKKKKK-----KKK-----KK 374
gi|7106107| 327 EMQST-IPKRSSLIMFDYYPVLVIFCKLFIHYNERFHYLIDTDRAIDLFIFLILYSFEY 385
gi|6648087| 410 EVSAISATISIVQKPNIAFETILFLWQAILYNKRFRFLITSFYATEFITSIQFYALRY 469

NOV5A 386 RADQSRVGLMHIGVFILLLLSGERNFGVRLN---KPYSIRVPMIPVFTGTHADLLIVV 441
gi|7303477| 394 RADQSRVGLMHIGVFILLLLSGERNFGVRLN---KAYSATVPMIPVFTGTHADLLITV 449
gi|7505130| 375 RNDSGRVGLIHMGVFIILLLLSGERNFGVRLN---KPYTAKANINVQTFGTADLLILV 430
gi|11360052| 375 KKKKKK----- 380
gi|7106107| 386 LGDPSTYNHLKLCVILLKRLTAEKYFCKRLNKPFQQTALPISMPVPFEGGTADFTLIA 445
gi|6648087| 470 REDNEHSGIVRICLFTIVHYLSCEKVLCEKLRNCMNQAQSLMSSLGFSVPMPMSYAEFLIIS 529

NOV5A 442 FHKIITSQHQRLOQIFDCILITIVNVSPYLKSLSMVTANKLHLLEAFSTTWFLFSAAQN 501
gi|7303477| 450 FHKIATGQHQRLOQIFDCILITILVNVSPYLKSLSMVASVKMLHLLEAFSTPWFLFSAPS 509
gi|7505130| 431 IHKLITGNYRLOQIFDCILITIMNVSPYMKSLSMVAANKLVHLEAFSTPWFLFSAPT 490
gi|11360052| 380 ----- 380
gi|7106107| 446 ISLLVQYTKDYHSEIAQMLCCSLCYLCLYAQNLSHSSQSILFELFQSAFPGFLLSNDVN 505
gi|6648087| 530 SFHISAVKRSPFSSLSPIVLTICNIAPFVENLSFVTCAKIMOLCSSLSRPFILFRNPRN 589

NOV5A 502 HHIVFFLLLEVFNNIIQYQFDGNSNLVYATIRKRSIFHQLANLPTDPTTIKALQRRRR-- 559
gi|7303477| 510 HHIVFFLLLEIFNNIIQYQFDGNSNLVYTIIRKRHVPHAMANLPTDMAGIAKCLSGRKTGG 569
gi|7505130| 491 POLVFSLLLEVFNNIIQYQFDGNSNLVYTIIRKRVFYQLSNLSTDAASIAKTLGRKSS-- 548
gi|11360052| 380 ----- 380
gi|7106107| 506 HKILKYVIGAINNALQYQAQYNAPLLYFFSMHKDYIEAVSALSPDAIMSVRNSSAEGDS- 564
gi|6648087| 590 HLLLEYLLQAISSIVENKFSQNPMLSSTIRLQQVFLNLSMKLPAVAQTKSQPLVALN- 648

NOV5A 559 -----TPEPLSRGTG 568
gi|7303477| 570 KFNLRPRVPQRRTPAVSQELPSAHVPEEYNEDEDEDEEBEINEEPKAEEDLESETESHER 629
gi|7505130| 548 -----KSNRND 554
gi|11360052| 380 ----- 380
gi|7106107| 564 -----AYWTRNCKTFSSKAFDSILLSR 586
gi|6648087| 648 -----SEGSSDFE---SKSSDNSTSLDGTPLQNTDF 675

NOV5A 569 SQEGTSMEGSRPAAPAEPTLKTSLVATPGIDKITEKSQVSEDGT-----LRS 616
gi|7303477| 630 SQAGELQSDVLTQAAPAEPTLKTSLLDTPGITOMTEREQAHPNDKQVEDSTDIVPYDRS 689
gi|7505130| 555 EMVDQLKSPSTAPPEIPAADAPAAQTLGGVSTTIG----- 590
gi|11360052| 380 ----- 380
gi|7106107| 587 LRYVRSKSPTPYYPPIESSEFGFTNLKDVTSKDEITDGFDAKALRSNLSRTHRDSRPVQPLL 646
gi|6648087| 676 KKVATVEDDSPFDELDFSSPFSSSSSRGCLSHISSRNVSISVPTVLQDVFSD---SPLV 732

NOV5A 617 LEPEPQOSLEDGSPAKGEPSQAWREQRRPSTS---SASQWSPTEPWLSSWKSPLQIOT 672
gi|7303477| 690 AASTPTDERKSTSPTELSRLSVAHRASIRMVP---GESDRWTPTEPWLSSWKSPLQIOT 745
gi|7505130| 590 -----LAATPALASMTGNVGNWEERPES---SQDNEWIATQEWADAWKSPLQIOT 637
gi|11360052| 380 ----- 380
gi|7106107| 647 KQRPQLHRALTESATLHGNDRLSDTDEAKVEPIAHSDVYTFKPTVEWNNKWPSPINFR 706
gi|6648087| 733 LSRKLKRGKIPENVSSSELIKCCASNPFKGDLE---IDSNLFAPSNWFWNSWHSRLEBDS 788

NOV5A 673 IMRLIQVIVPQVEKICIDKGLTDESEILRFQHGTVGLLE-VHPILIRKYQANS GTAM 731

A disclosed NOV6a nucleic acid of 1116 nucleotides (also referred to as SC134912642_da1) encoding a novel Synaptotagmin-like protein is shown in Table 6A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 1114-1116. The start and stop codons are in bold letters in Table 6A.

Table 6A. NOV6a Nucleotide Sequence (SEQ ID NO:13)

ATGTACCGGGACCCGGAGGCGGCCAGCCAGGTGCGCCCTCGCGCAGCTCCTGCTGGTCTCTGCCATCATCA
 CCGTCAGCCTTAGCGTCACTGTCGTCCTCGCTAGCCGGTGCCACTGGTGTCAAGCGCAAACCTGGGCAAACGCTA
 CAAGAATTCTTGGAGACGGTGGGCACGCCAGACTCAGGACGTGGGCGCAGTGAGAAGAAGGCTATCAAGTTG
 CCTGCAGGAGGGAAGGCGGTGAACACAGCCCCCGTCCAGGCCAGACACCCACGATGAGTCCGACCGCCGGA
 CCGAGCCACGTTCCTCCTTCTCAGACCTCGTCAACTCCCTCACCAGCGAGATGCTCATGGAGTCCACGCTCAC
 CGTGAAGATCATGAAGGCCAGGAGCTGCCGGCCAAGGACTTCAGCGGCACCAGCGACCCCTTCGTCAAGATC
 TACCTGCTGCCCGACAAGAAGCAAGCTGGAGACCAAGGTGAAGCGGAAGAACCTGAACCCCACTGGAACG
 AGACCTTCCTCTTTGAAGTTTTCCCTATGAGAAGGTGGTGCAGAGGATCCTCTACCTCCAAGTCTGGACTA
 TGACCGCTTCAGCCGCCACGACCCATTGGGGAGGTGTCCATCCCCCTTAACAGGTGGACCTGACCCAGATG
 CAGATCTGGAAGGATCTGAAGCCATGCAGCGATGGGAGTGGGAGCCGAGGGGAGCTGCTCTTGCTCTCTGCT
 ACAACCCCTCTGCCAACTCCATCATCGTGAACATCATCAAGCCCGGAACCTCAAGCCATGGACATCGGGGG
 CACATCAGACCCCTACGTGAAGGTATGGCTGATGTACAAGGACAAGCGGGTGGAGAAGAAGACGGTGACG
 ATGAAGAGGAACCTGAACCCCATCTTCAATGAGTCTTCGCCTTCGATATCCCCACGGAGAAGCTGAGGGAGA
 CGACCATCATCATCACTGTCTATGGACAAGGACAAGCTCAGCCGAATGACGTCATCGGCAAGATCTACCTGTC
 CTGGAAGAGCGGGCCAGGGGAGGTGAAGCACTGGAAGGACATGATTGCCCTCCCGGCAGCCCGTGGCCAG
 TGGCACCAGCTGAAGGCTGA

The NOV6a nucleic acid was identified on chromosome 11q12.2 and has 709 of 768 bases (92%) identical to a *Mus musculus* synaptotagmin VII mRNA (gb:GENBANK-ID:AB026804|acc:AB026804) ($E = 1.3e^{-208}$).

A disclosed NOV6a polypeptide (SEQ ID NO:14) encoded by SEQ ID NO:13 is 371 amino acid residues and is presented using the one-letter code in Table 6B. Signal P, Psort and/or Hydropathy results predict that NOV6a contains a signal peptide and is likely to be localized in the cytoplasm with a certainty of 0.8200. The most likely cleavage site for a NOV6a peptide is between amino acids 35 and 36, at: VLA-SR.

Table 6B. Encoded NOV6a protein sequence (SEQ ID NO:14)

MYRDPEAASPGAPSRDVLVSAIITVLSVTVVLASRCHWCQRKLGKRYKNSLETVGTPDSDGRGRSEKKAIK
 LPAGGKAVNTAPVPGQTPHDESDRRTEPRSSFSDLVNSLTSEMLMESTLTVKIMKAQELPAKDFSGTSDPFV
 KIYLLPDKKHKLETKVKKRNLNPHWNETFLFEGFPYEKVVQRILYLQVLDYDRFSRHDPIGEVSIPLKQVDL
 TQMQUIWDLKPCSDGSGSRGELLLSLCYNPSANSIIIVNIIKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKK
 KTVTMKRNLNPIFNESFAFDIPTKLRRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDMIARPR
 QPVAQWHQLKA

The NOV6a amino acid sequence has 248 of 255 amino acid residues (97%) identical to, and 251 of 255 amino acid residues (98%) similar to, a *Rattus norvegicus* 403 amino acid residue synaptotagmin VII protein (ptnr:SPTREMBL-ACC:Q62747) ($E = 1.3^{-190}$).

NOV6a is expressed in at least the following tissues: Adrenal Gland/Suprarenal gland, Bone, Brain, Cerebral Medulla/Cerebral white matter, Heart, Hippocampus, Liver, Mammary gland/Breast, Pituitary Gland, Placenta, Salivary Glands, Thalamus. This information was

derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

NOV6b

A disclosed NOV6b nucleic acid of 1212 nucleotides (also referred to as CG56106-01) encoding a novel Synaptotagmin-like protein is shown in Table 6C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 1210-1212. The start and stop codons are in bold letters in Table 6C.

Table 6C. NOV6b Nucleotide Sequence (SEQ ID NO:15)
ATGTACCGGGACCCGGAGGCGGCCAGCCCAGGGGCGCCCTCGCGCGACGTCTGCTGGTCTCTGCCATCA TCACCGTCAGCCTTAGCGTCACTGTCGTCCTCTGCGGCCTCTGCCACTGGTGTGTCAGCGCAAACCTGGGCAA ACGCTACAAGAATTCCTTGGAGACGGTGGGCACGCCAGACTCAGGGCGTGGGCGCACTGAGAAGAAGGCT ATCAAGTTGCTGTCAGGAGGAAGGCGGTGAACACAGCCCCCGTCCAGGCCAGACACCCACGATGAGT CCGACCGCCGGACCGAGCCACGTTCCCTCCGTCTCAGACCTCGTCAACTCCCTCACCAGCGAGATGCTCAT GCTCTCCCCAGGCTCCGAGGAGGATGAGGCCACGAGGGTTCAGCCGAGAGAACCTGGGCGGATCCAG TTCAGTGTGCGCTACAACCTCCAGGAGTCCACGCTCACCGTGAAGATCATGAAGGCCAGGAGCTGCCGG CCAAGGACTTCAGCGGCACCGAGCCACCCCTTCGTCAAGATCTACCTGCTGCCCCACAAGAAGCACAAAGCT GGAGACCAAGGTGAAGCGGAAGAACCTGAACCCCACTGGAACGAGACCTTCCTCTTTGAAGGTTTTCCC TATGAGAAGGTGGTGCAGAGGATCCTCTACCTCCAAGTCTTGACTATGACCGCTTCAGCCGCAACGACC CCATTGGGGAGGTGCCATCCCCCTTAACAAGGTGGACCTGACCCAGATGCAGACCTTCTGGAAGGATCT GAAGCCATGCAGCGATGGGAGTGGGAGCCGAGGGAGCTGCTCTGTCTCTCTGTACAACCCCTCTGCC AACTCCATCATCGTGAACATCATCAAAGCCCGGAACCTCAAAGCCATGGACATCGGGGGACATCAGACC CCTACGTGAAGGTATGGCTGATGTACAAGGACAAGCGGTGGAGAAGAAGAAGACGGTGACGATGAAGAG GAACCTGAACCCCATCTTCAATGAGTCTTCGCCTTCGATATCCCCACGGAGAAGCTGAGGGAGACGACC ATCATCATCACTGTATGACAAGGACAAGCTCAGCCGCAATGACGTATCGGCAAGATCTACCTGTCTCT GGAAGAGCGGGCCAGGGAGGTGAAGCACTGGAAGGACATGATTGCCCGTCCCCGGCAGCCGCTGGCCCA GTGGCACCAGCTGAAGGCCTGA

The NOV6b nucleic acid was identified on chromosome 11q12-13.1 and has 1201 of 1212 bases (99%) identical to a *Homo sapiens* synaptotagmin VII mRNA (gb:GENBANK-ID:AF038535|acc:AF038535.1) ($E = 5.6e^{-263}$)

A disclosed NOV6b polypeptide (SEQ ID NO:16) encoded by SEQ ID NO:15 is 403 amino acid residues and is presented using the one-letter code in Table 6D. Signal P, Psort and/or Hydropathy results predict that NOV6b contains a signal peptide and is likely to be localized in the endoplasmic reticulum (membrane) with a certainty of 0.8200 and the plasma membrane with a certainty of 0.5140. The most likely cleavage site for a NOV6b peptide is between amino acids 46 and 47, at: KLG-KR.

Table 6D. Encoded NOV6b protein sequence (SEQ ID NO:16).
MYRDPEASPGAPSRDVLVSAIITVSLSVTVVLCGLCHWCQRKLGKRYKNSLETVGTDPDGRGRSEKKAIKLPA GGKAVNTAPVPGQTPHDESDRTEPRSSVSDLVNSLTSEMLMLSPGSEDEAHEGCSRENLGRIQFSVGYNFQES TLTVKIMKAQELPAKDFSGTSDPFVKIYLLPDKKKHLETKVKKRNLNPHWNETFLFEGFPYEKVVQRILYLQVLD YDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSIIVNIIKARNLKAMDIGG TSDPYVKVWLMYKDKRVEKKKVTMKNLNPINFESFAFDIPEKLRETTIITVMDKDKLSRNDVIGKIYLSWK

The NOV6b amino acid sequence has 398 of 403 amino acid residues (98%) identical to, and 401 of 403 amino acid residues (99%) similar to, a *Rattus norvegicus* 403 amino acid residue synaptotagmin VII protein (ptnr:SPTREMBL-ACC:Q62747) ($E = 7.1e^{-217}$).

NOV6b is expressed in at least the following tissues: Adrenal Gland/Suprarenal gland, Bone, Brain, Cerebral Medulla/Cerebral white matter, Heart, Hippocampus, Liver, Mammary gland/Breast, Pituitary Gland, Placenta, Salivary Glands, Thalamus. This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

NOV6a and NOV6b are very closely homologous as is shown in the amino acid alignment in Table 6E.

Table 6E Amino Acid Alignment of NOV6a and NOV6b

	10	20	30	40	50
NOV6a	MYRDPEAASPGAPSRDVLVSAIITVSLSVTVVLASRCHWCQKRLGKRYK				
NOV6b	MYRDPEAASPGAPSRDVLVSAIITVSLSVTVVL	CGLCHWCQKRLGKRYK			
	60	70	80	90	100
NOV6a	NSLETVGTPDSGRGRSEKKAIKLPAGGKAVNTAPVPGQTPHDESDRRTEP				
NOV6b	NSLETVGTPDSGRGRSEKKAIKLPAGGKAVNTAPVPGQTPHDESDRRTEP				
	110	120	130	140	150
NOV6a	RSSFSDLVNSLTSEMLMES				
NOV6b	RSSFSDLVNSLTSEMLMES	PGSEDEAHEGCSRENLGRIQFSVGYNFQES			
	160	170	180	190	200
NOV6a	TLTVKIMKAQELPAKDFSGTSDPFVKIYLLPDKKHKLETQVKKRNLP				
NOV6b	TLTVKIMKAQELPAKDFSGTSDPFVKIYLLPDKKHKLETQVKKRNLP				
	210	220	230	240	250
NOV6a	NETFLFEGFPYEKVVQRIYLYQVLDYDRFSRNDPIGEVSIPLKQVDLTQM				
NOV6b	NETFLFEGFPYEKVVQRIYLYQVLDYDRFSRNDPIGEVSIPLKQVDLTQM				
	260	270	280	290	300
NOV6a	Q-IWKDLKPCSDGSGRGELLLSLCYNPSANSIIVNIIKARNLKAMDIGG				
NOV6b	QTFWKDLKPCSDGSGRGELLLSLCYNPSANSIIVNIIKARNLKAMDIGG				
	310	320	330	340	350
NOV6a	TSDPYVKVWLMYKDKRVEKKKTVTMKNLNPINFESFAFDIPTTEKLRETT				
NOV6b	TSDPYVKVWLMYKDKRVEKKKTVTMKNLNPINFESFAFDIPTTEKLRETT				
	360	370	380	390	400
NOV6a	IIITVMDKDKLSRNDVIGKIYLSWKSGPGEVKHWKDMIARPRQPVAQWHQ				
NOV6b	IIITVMDKDKLSRNDVIGKIYLSWKSGPGEVKHWKDMIARPRQPVAQWHQ				
NOV6a	LKA				
NOV6b	LKA				

Homologies to any of the above NOV6 proteins will be shared by the other NOV6 proteins insofar as they are homologous to each other as shown above. Any reference to NOV6 is assumed to refer to both of the NOV6 proteins in general, unless otherwise noted.

NOV6a also has homology to the amino acid sequences shown in the BLASTP data listed in Table 6F.

Table 6F. BLAST results for NOV6a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 11067375 ref NP_067691.1	synaptotagmin 7 [Rattus norvegicus]	403	358/403 (88%)	363/403 (89%)	0.0
gi 9055364 ref NP_061271.1	synaptotagmin 7 [Mus musculus]	403	356/403 (88%)	362/403 (89%)	0.0
gi 2724126 gb AAB92667.1 (AF038535)	synaptotagmin VII [Homo sapiens]	418	350/403 (86%)	356/403 (87%)	0.0
gi 12667450 gb AAK01451.1 AF336856.1 (AF336856)	synaptotagmin VIIa [Rattus norvegicus]	520	296/351 (84%)	304/351 (86%)	1e-159
gi 12667458 gb AAK01455.1 AF336860.1 (AF336860)	synaptotagmin VIIe [Rattus norvegicus]	643	296/351 (84%)	304/351 (86%)	1e-159

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 6G.

Table 6G Information for the ClustalW proteins

- 1) NOV6a (SEQ ID NO:14)
- 2) gi|11067375|ref|NP_067691.1| synaptotagmin 7 [Rattus norvegicus] (SEQ ID NO:60)
- 3) gi|9055364|ref|NP_061271.1| synaptotagmin 7 [Mus musculus] (SEQ ID NO:61)
- 4) gi|1171691|sp|P42676|NEUL RAT NEUROLYSIN PRECURSOR (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) [Rattus norvegicus] (SEQ ID NO:62)
- 5) gi|12667450|gb|AAK01451.1|AF336856.1 (AF336856) synaptotagmin VIIa [Rattus norvegicus] (SEQ ID NO:63)
- 6) gi|12667458|gb|AAK01455.1|AF336860.1 (AF336860) synaptotagmin VIIe [Rattus norvegicus] (SEQ ID NO:64)

NOV6A	1	-----MYRDPEAASPGAPSRDVLVLSAII TVSLSVTVVLASRCHWCQRK	44
gi 11067375	1	-----MYRDPEAASPGAPTRDVLVLSAII TVSLSVTVVLCGLCHWCQRK	44
gi 9055364	1	-----MYRDPEAASPGAPTRDVLVLSAII TVSLSVTVVLCGLCHWCQRK	44
gi 2724126	1	AGYLQEPGXLSXXGTM YRDPRRPARCX-LADVLVLSAII TVSLSVTVVLCGLCHWCQRK	59
gi 12667450	1	-----MYRDPEAASPGAPTRDVLVLSAII TVSLSVTVVLCGLCHWCQRK	44
gi 12667458	1	-----MYRDPEAASPGAPTRDVLVLSAII TVSLSVTVVLCGLCHWCQRK	44
NOV6A	45	LGKRYKNSLETVGTPDSCGRGRSEKKAI-----K-----	72
gi 11067375	45	LGKRYKNSLETVGTPDSCGRGRSEKKAI-----K-----	72
gi 9055364	45	LGKRYKNSLETVGTPDSCGRGRSEKKAI-----K-----	72
gi 2724126	60	LGKRYKNSLETVGTPDSCGRGRSEKKAI-----K-----	87
gi 12667450	45	LGKRYKNSLETVGTPDSCGRGRSEKKAINGTLLSGAKVATAAAGLAVEREGR LGKPPAPVP	104
gi 12667458	45	LGKRYKNSLETVGTPDSCGRGRSEKKAINGTLLSGAKVATAAAGLAVEREGR LGKPPAPVP	104
NOV6A	72	-----	72
gi 11067375	72	-----	72
gi 9055364	72	-----	72
gi 2724126	87	-----	87
gi 12667450	105	PPGEDALRSGGAAPSEPGSSGKAGRGRWRMVQSHLAAGKLNLS-----	147
gi 12667458	105	PPGEDALRSGGAAPSEPGSSGKAGRGRWRMVQSHLAAGKLNLSNFEDSTLSTATTLESIP	164

NOV6A	72	-----	72
gi 11067375	72	-----	72
gi 9055364	72	-----	72
gi 2724126	87	-----	87
gi 12667450	147	-----	147
gi 12667458	165	SSAGEPKCQRPTLMRQQSLQQLSQNRGRQPSQPTTSQSLGQLQAHASAPGSNP	224
NOV6A	72	-----	72
gi 11067375	72	-----	72
gi 9055364	72	-----	72
gi 2724126	87	-----	87
gi 12667450	147	-----KEGRMVVLSLVLGL	161
gi 12667458	225	GRGQARQGTSAAGGRSRNPGSWDHVVGQIRNRGLDMKSFLEGRMVVLSLVLGL	284
NOV6A	72	-----LPAGGKAVNTAPVPGQTPHDESDRRTPEPRSS	104
gi 11067375	72	-----LPAGGKAVNTAPVPGQTPHDESDRRTPEPRSS	104
gi 9055364	72	-----LPAGGKAVNTAPVPGQTPHDESDRRTPEPRSS	104
gi 2724126	87	-----LPAGGKAVNTAPVPGQTPHDESDRRTPEPRSS	119
gi 12667450	162	SEQDDFANIPDLQNPQTQONQNAQGDKRLPAGGKAVNTAPVPGQTPHDESDRRTPEPRSS	221
gi 12667458	285	SEQDDFANIPDLQNPQTQONQNAQGDKRLPAGGKAVNTAPVPGQTPHDESDRRTPEPRSS	344
NOV6A	105	-----ESTLTVKIMKAQELPA	133
gi 11067375	105	SDLVNSLTSEMLMLSPGSEDEAHEGCSRENLGRIQFSVGYNFQESTLTVKIMKAQELPA	164
gi 9055364	105	SDLVNSLTSEMLMLSPGSEDEAHEGCSRENLGRIQFSVGYNFQESTLTVKIMKAQELPA	164
gi 2724126	120	SDLVNSLTSEMLMLSPGSEDEAHEGCSRENLGRIQFSVGYNFQESTLTVKIMKAQELPA	179
gi 12667450	222	SDLVNSLTSEMLMLSPGSEDEAHEGCSRENLGRIQFSVGYNFQESTLTVKIMKAQELPA	281
gi 12667458	345	SDLVNSLTSEMLMLSPGSEDEAHEGCSRENLGRIQFSVGYNFQESTLTVKIMKAQELPA	404
NOV6A	134	KDFSGTSDPFVKIYLLPDKKHKLETKVKRKQNLNPHWNETFLFEGFPYEKVVQRILYLQVL	193
gi 11067375	165	KDFSGTSDPFVKIYLLPDKKHKLETKVKRKQNLNPHWNETFLFEGFPYEKVVQRILYLQVL	224
gi 9055364	165	KDFSGTSDPFVKIYLLPDKKHKLETKVKRKQNLNPHWNETFLFEGFPYEKVVQRILYLQVL	224
gi 2724126	180	KDFSGTSDPFVKIYLLPDKKHKLETKVKRKQNLNPHWNETFLFEGFPYEKVVQRILYLQVL	239
gi 12667450	282	KDFSGTSDPFVKIYLLPDKKHKLETKVKRKQNLNPHWNETFLFEGFPYEKVVQRILYLQVL	341
gi 12667458	405	KDFSGTSDPFVKIYLLPDKKHKLETKVKRKQNLNPHWNETFLFEGFPYEKVVQRILYLQVL	464
NOV6A	194	DYDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSII	252
gi 11067375	225	DYDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSII	284
gi 9055364	225	DYDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSII	284
gi 2724126	240	DYDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSII	299
gi 12667450	342	DYDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSII	401
gi 12667458	465	DYDRFSRNDPIGEVSIPLNKVDLTQMOTFWKDLKPCSDGSGSRGELLLSLCYNPSANSII	524
NOV6A	253	VNI IKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKKKTVTKRNLNPIFNESFAFDIPE	312
gi 11067375	285	VNI IKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKKKTVTKRNLNPIFNESFAFDIPE	344
gi 9055364	285	VNI IKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKKKTVTKRNLNPIFNESFAFDIPE	344
gi 2724126	300	VNI IKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKKKTVTKRNLNPIFNESFAFDIPE	359
gi 12667450	402	VNI IKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKKKTVTKRNLNPIFNESFAFDIPE	461
gi 12667458	525	VNI IKARNLKAMDIGGTSDPYVKVWLMYKDKRVEKKKTVTKRNLNPIFNESFAFDIPE	584
NOV6A	313	KLRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDIARPROPVAQWHLKA	371
gi 11067375	345	KLRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDIARPROPVAQWHLKA	403
gi 9055364	345	KLRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDIARPROPVAQWHLKA	403
gi 2724126	360	KLRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDIARPROPVAQWHLKA	418
gi 12667450	462	KLRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDIARPROPVAQWHLKA	520
gi 12667458	585	KLRETTIIITVMDKDKLSRNDVIGKIYLSWKS GPGEVKHWKMDIARPROPVAQWHLKA	643

Table 6H-6K lists the domain description from DOMAIN analysis results against NOV6a. This indicates that the NOV6a sequence has properties similar to those of other proteins known to contain this domain.

[illegible]

gn1|Smart|smart00239, C2, Protein kinase C conserved region 2 (CaLB); Ca2+-binding motif present in phospholipases, protein kinases C, and synaptotamins (among others). Some do not appear to contain Ca2+-binding sites. Particular C2s appear to bind phospholipids, inositol polyphosphates, and intracellular proteins. Unusual occurrence in perforin. Synaptotagmin and PLC C2s are permuted in sequence with respect to N- and C-terminal beta strands. SMART detects C2 domains using one or both of two profiles.. (SEQ ID NO:94)

Length = 101 residues, 99.0% aligned

Score = 103 bits (258), Expect = 1e-23

NOV6a	120	TLTVKIMKAQELPAKDFSGTSDPFVKIYLLPDKKKHLETKVKRKNLNPHWNETFLFEGFP	179
		+ + + + + + +	
00239	1	TLTVKIISARNLPPKDKGGKSDPYKVSLDGDPREKKKTKVVKNTLNPVWNETFEFEVFP	60
NOV6a	180	YEKVVQRILYLQVLDYDRFSRHDPIGEVSIPLKQVDLTQMQUIW	222
		++ +	
00239	61	PE---LSELEIEVDKDRFSRDDFIGRVTIPLSDLLGGRHEK	100

Table 6I. Domain Analysis of NOV6a

gnl|Smart|smart00239 (SEQ ID NO:94)
Length = 101 residues, 96.0% aligned
Score = 91.3 bits (225), Expect = 9e-20

[illegible]

Table 6J. Domain Analysis of NOV6a

gnl|Pfam|pfam00168, C2, C2 domain. (SEQ ID NO:95)
Length = 88 residues, 98.9% aligned
Score = 98.6 bits (244), Expect = 6e-22

NOV6a 121 LTVKIMKAQELPAKDFSGTSDPFVKIYLLPDKK--HKLETKVKRKNLNPHWNNETFLFEGF 178
 |||++|+|||+|||+|+|||+||+|||+|||+|||+|||+|||
 00168 1 LTVKVISARNLPKMDMNGLSDPYVKVDLDGDPKDTKKFKTKTKVKKTLNPNVWNETFVFEKV 60

The above defined information for NOV6 suggests that NOV6 may function as a member of a synaptotagmin family. Therefore, the NOV6 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the NOV6 compositions of the present invention will have efficacy for treatment of patients suffering from Atopy; Osteoporosis-pseudoglioma syndrome; Smith-Lemli-Opitz syndrome, type I; Smith-Lemli-Opitz syndrome, type II; Xeroderma pigmentosum, group E, subtype 2; Asthma, atopic, susceptibility to; Diabetes mellitus, insulin-dependent, 4; Susceptibility to IDDM; Angioedema, hereditary; Paraganglioma, familial nonchromaffin, 2; Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection; metabolic disorders and Lambert-Eaton myasthenic syndrome. The NOV6 nucleic acid encoding synaptotagmin-like protein, and the synaptotagmin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV7

A disclosed NOV7 nucleic acid of 1164 nucleotides (also referred to wugc_draft_h_nh0781m21_20000809_da1) encoding a novel Serine Protease TLSP-like receptor protein is shown in Table 7A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 113-115 and ending with a TAG codon at nucleotides 854-856. Putative untranslated regions are found upstream from the initiation codon and downstream from the termination codon in Table 7A, and the start and stop codons are in bold letters.

Table 7A. NOV7 Nucleotide Sequence (SEQ ID NO:17)

CTGCCTTGCTCCACACCTGGTCAGGGGAGAGAGGGGAGGAAAGCCAAAGGAAGGGACCTAACTGAAAACAA
ACAAGCTGGGAGAAGCAGGAATCTGCGCTCGGGTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGG
AAGTCATCGGGCAGAGGTCTCACAGCAGCCAAGGAACCTGGGGCCCGTCTCTCCCCCTCCAGGCCATGAG
GATTCTGCAGTTAATCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGT
TCGAGTGAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGGGGCG
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCCTCCCAACAAAGACCGCG
CAATGACATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCT
CCTCACGCTGTGCTACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCAGTTA
CGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCC
CGGCAACATCACAGACACCTTGGTGTGTGCCAGCTGCAGGAAGGGGCAAGGACTCCTGCCAGGGTGACT
CCGGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTGGGGCCAGGATCCGTGTGCGATC
ACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTGGTCTGGATCCAGGAGACGATTAAGAACAA
TTAGGCTGGACCCACCCACAGCCCATCACCCTCCATTTCACCTGGTGTGTTGGTTCTGTTCACCTCTG
TTAATAAGAAACCCTAAGCCAAGACCCCTCTACGAACATTCTTTGGGCCCTCTGGACTACAGGAGATGCTGT
CACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGAC
TCTGGGAATGACAACACCTGGTTTGTGTTTTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCATATAT

CAAGGTTTCAATAAATATTTGCTAAATG

The disclosed NOV7 nucleic acid sequence, localized to chromosome 19, has 531 of 607 bases (87%) identical to a *Homo sapiens* trypsin-like serine protease (TLSP) mRNA (gb:GENBANK-ID:AF164623|acc:AF164623) ($E = 1.3e^{-165}$).

A disclosed NOV7 polypeptide (SEQ ID NO:18) encoded by SEQ ID NO:17 is 247 amino acid residues and is presented using the one-letter amino acid code in Table 7B. Signal P, Psort and/or Hydropathy results predict that NOV7 contains a signal peptide and is likely to be localized in the mitochondrial inner membrane with a certainty of 0.6921 and to the plasma membrane with a certainty of 0.6500. The most likely cleavage site for a NOV7 peptide is between amino acids 50 and 51, at: VGG-ET.

Table 7B. Encoded NOV7 protein sequence (SEQ ID NO:18).

MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAMRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAAL
FEKTRLLCGATLIAPRWLLTAAHCLKPLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCCLIS
GWGSTSSPQLRLPHTLRCANITIEHQKCNAYPGNITDTMVCASVQEGGKDSQCQDGGPLVCNQSLQGI
ISWGQDPCAITRKPGVYTKVCKYVWVIQETIKNN

The NOV7 amino acid sequence has 146 of 149 amino acid residues (97%) identical to, and 147 of 149 amino acid residues (98%) similar to the *Homo Sapiens* 282 amino acid residue serine protease (TLSP) protein (ptnr:SPTREMBL-ACC:O75837) ($E = 5.2e^{-131}$).

NOV7 is a spliced isoform of the serine protease (TLSP) from *Homo sapiens* (GenBank ID: AB012917). It is missing 105 nucleotides between positions 406 and 407. Deletion of this exon resulted in a deletion of 35 amino acid residues between positions 98 and 99 in the protein sequence.

NOV7 is expressed in at least the following tissues: Colon, Heart, Lung, Ovary, Parotid Salivary glands, Prostate, Salivary Glands, Stomach (normal), Stomach (poorly differentiated adenocarcinoma with signet ring cell) Testis and Uterus. In addition, the sequence is predicted to be expressed in the following tissues/cell lines because of the expression pattern of a closely related *Homo sapiens* trypsin-like serine protease (TLSP) gene homolog (GENBANK-ID: gb:GENBANK-ID:AF164623|acc:AF164623):brain, thymus, spleen, liver and in breast carcinoma cell line BT-474.

NOV7 also has homology to the amino acid sequence shown in the BLASTP data listed in Table 7C.

Table 7C. BLAST results for NOV7

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
------------------------	-------------------	-------------	--------------	---------------	--------

gi_3649791 dbj_BAA33404.1 (AB012917)	serine protease (TLSP) [Homo sapiens]	282	244/282 (86%)	245/282 (86%)	1e-124
gi_5803199 ref_NP_006844.1	kallikrein 11; protease, serine, trypsin-like; protease, serine, 20 trypsin-like [Homo sapiens]	250	212/250 (84%)	213/250 (84%)	1e-107
gi_6681654 dbj_BAA36955.1 (AB016227)	hippostasin prostate type [Mus musculus]	276	191/282 (67%)	214/282 (75%)	1e-101
gi_9910298 ref_NP_064358.1	protease, serine, 20; hippostasin [Mus musculus]	249	175/248 (70%)	194/248 (77%)	5e-96
gi_9296988 sp Q9UKQ9 KLK9_HUMAN	kallikrein 9 precursor (kallikrein-like protein 3) (KLK-L3) [Homo sapiens]	250	117/242 (48%)	152/242 (62%)	7e-57

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 7D.

Table 7D. Information for the ClustalW proteins

- 1) NOV7 (SEQ ID NO:18)
- 2) gi_3649791|dbj_BAA33404.1| (AB012917) serine protease (TLSP) [Homo sapiens] (SEQ ID NO:65)
- 3) gi_5803199|ref_NP_006844.1| kallikrein 11; protease, serine, trypsin-like; protease, serine, 20 trypsin-like [Homo sapiens] (SEQ ID NO:66)
- 4) gi_6681654|dbj_BAA36955.1| (AB016227) hippostasin prostate type [Mus musculus] (SEQ ID NO:67)
- 5) gi_9910298|ref_NP_064358.1| protease, serine, 20; hippostasin [Mus musculus] (SEQ ID NO:68)
- 6) gi_9296988|sp|Q9UKQ9|KLK9_HUMAN kallikrein 9 precursor (kallikrein-like protein 3) (KLK-L3) [Homo sapiens] (SEQ ID NO:69)

NOV7	1	MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAMRIQLILLALATGLVGGETRIIKGFEC	60
gi_3649791	1	MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAMRIQLILLALATGLVGGETRIIKGFEC	60
gi_5803199	1	-----MRILQLILLALATGLVGGETRIIKGFEC	28
gi_6681654	1	-----MRRLKSDWKLSTETREPGARPALLQARMILRLIALALVTGHVGGETRIIKGFEC	54
gi_9910298	1	-----MLRLIALALVTGHVGGETRIIKGFEC	27
gi_9296988	1	-----MKLGLLCALLSLLAGHGWDTRAIGAECC	29
NOV7	61	KPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRVIVHLCOHNLQKEEGCEQTRT	98
gi_3649791	61	KPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRVIVHLCOHNLQKEEGCEQTRT	120
gi_5803199	29	KPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRVIVHLCOHNLQKEEGCEQTRT	88
gi_6681654	55	RPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCKRPHVILLGEBHLEKTDGCEQRRM	114
gi_9910298	28	RPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCKRPHVILLGEBHLEKTDGCEQRRM	87
gi_9296988	30	RPNSQPWQAALFEHLTRLFCGATLISDRWLLTAAHCKRPLYLWVRLGEBHLEKTDGCEQRRM	89
NOV7	98	-----LPNKDRNDIMLVKMASPVSTTAVRPLTLSSRCVTAAGTSCCLISGWG	145
gi_3649791	121	ATESFPHPGFFNNSLPNKDRNDIMLVKMASPVSTTAVRPLTLSSRCVTAAGTSCCLISGWG	180
gi_5803199	89	ATESFPHPGFFNNSLPNKDRNDIMLVKMASPVSTTAVRPLTLSSRCVTAAGTSCCLISGWG	148
gi_6681654	115	ATESFPHPDFFNNSLPNKDRNDIMLVKMASPVSTTAVRPLTLSPHCVAAGTSCCLISGWG	174
gi_9910298	88	ATESFPHPDFFNNSLPNKDRNDIMLVKMASPVSTTAVRPLTLSPHCVAAGTSCCLISGWG	147
gi_9296988	90	VTDFFPHPGFFNKDLSANDHNDIMLIRLPRQARLSPAVQPLNLSQTCVSPCMQCLISGWG	149
NOV7	146	STSSPQLRLPHTLRCAITIIIEHKCEKAYPGNITDTMVCASVQEGGKDSQCGDSGGPLV	205
gi_3649791	181	STSSPQLRLPHTLRCAITIIIEHKCEKAYPGNITDTMVCASVQEGGKDSQCGDSGGPLV	240
gi_5803199	149	STSSPQLRLPHTLRCAITIIIEHKCEKAYPGNITDTMVCASVQEGGKDSQCGDSGGPLV	208
gi_6681654	175	TTSSPQLRLPHSLRCANVSIIEHKCEKAYPGNITDTMVCASVRKEGKDSQCGDSGGPLV	234
gi_9910298	148	TTSSPQLRLPHSLRCANVSIIEHKCEKAYPGNITDTMVCASVRKEGKDSQCGDSGGPLV	207
gi_9296988	150	AVSSPKALFPVTLQCANISILENKLCHWAYPGHISLSMLCAGLWEGGRGSCQCGDSGGPLV	209
NOV7	206	CNCSLQGIISWGQDPCATRKPGVYTKVCKYVVDWIOETIKNN	247
gi_3649791	241	CNCSLQGIISWGQDPCATRKPGVYTKVCKYVVDWIOETIKNN	282

The amino acid sequence of NOV7 has high homology to other proteins as shown in Table 7G.

Table 7G. BLASTX results for NOV7						
Sequences producing High-scoring Segment Pairs:				Reading High	Smallest Sum Prob	
				Frame	Score	P(N) N
patp:AA42439	CASB12 amino acid sequence,	Homo Sapi	282 aa..	+2	792	3.0e-130 1
patp:AAB11712	Huma serine protease BSSP6,	Homo Sapi	282 aa..	+2	792	3.0e-130 1
patp.AAY43636	Human prostate-associated serum protease,	Homo Sapi	282 aa..	+2	792	3.0e-130 1

The trypsin family is almost totally confined to animals, although trypsin-like enzymes are found in actinomycetes of the genera *Streptomyces* and *Saccharopolyspora*, and in the fungus *Fusarium oxysporum*. The enzymes are inherently secreted, being synthesised with a signal peptide that targets them to the secretory pathway. Animal enzymes are either secreted directly, packaged into vesicles for regulated secretion, or are retained in leukocyte granules.

Proteases play a pivotal role in several biologic processes, including tissue remodeling and cell migration. By PCR of human hippocampus cDNA using primers derived from mouse neuropsin cDNA sequences corresponding to conserved regions of serine proteases, a novel serine protease, KLK11, was identified which was named TLSP. The deduced 260-amino acid protein contains a signal peptide, 3 key amino acids essential for serine protease activity, an asp residue in a position that suggests a trypsin-type substrate specificity for basic amino acids at the P1 position, conserved amino acids that can form an oxyanion hole, and a potential N-glycosylation site. KLK11 shares 48% amino acid sequence identity with mouse neuropsin, 43% identity with both human trypsin-1 and human kallikrein, and 38% identity with the mouse nerve growth factor gamma subunit. Western blot analysis of recombinant KLK11 suggested that the protein is secreted and posttranslationally processed.

Proteolytic enzymes have been readily used in traditional medicine and studies have shown that enzyme therapy can reduce the adverse effects caused by radiotherapy and chemotherapy. There is also evidence that, in some types of tumours, survival may be prolonged. The beneficial effect of systemic enzyme therapy seems to be based on its anti-inflammatory potential (Leipner and Saller, *Drugs* 59(4):769-80, 2000).

The above defined information for NOV7 suggests that this NOV7 protein may function as a member of a Serine Protease TLSP family. Therefore, the NOV7 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the

NOV7 compositions of the present invention will have efficacy for treatment of patients suffering from cancer, neurological disorders, digestive system disorders and all or some of the protease/protease inhibitor deficiency disorders.. The NOV7 nucleic acid encoding Serine Protease TLSP-like protein, and the Serine Protease TLSP-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV8

NOV8 includes four novel Glypican-2 Precursor-like proteins disclosed below. The disclosed proteins have been named NOV8a, NOV8b, NOV8c and NOV8d.

NOV8a

A disclosed NOV8a nucleic acid of 1785 nucleotides (also referred to 134913441_EXT) encoding a novel Glypican-2 Precursor-like protein is shown in Table 8A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TAA codon at nucleotides 1738-1740. A putitive untranslated region downstream from the termination codon is underlined in Table 8A, and the start and stop codons are in bold letters.

Table 8A. NOV8a Nucleotide Sequence (SEQ ID NO:19)

ATGTCCGCGCTGCGACCTCTCCTGCTTCTGCTGCTGCCTCTGTGTCCCGGTCTGGTCCCGGACCCGGGAG
CGAGGCAAAGGTCACCCGAGTGTGTGACAGACCCGGCAGGTGCTGGGGGCCCGGGATATAGCTTAAACC
TAATCCCTCCCGCCTGATCTCAGGTGAGCACCTCCGGGTCTGTCCCAGGAGTACACCTGCTGTTCCAGT
GAGACAGAGCAGAGGCTGATCAGGGAGACTGAGGCCACCTTCCGAGGCCTGGTGGAGGACAGCGGCTCCTT
TCTGGTTCACACACTGGCTGCCAGGCACAGAAAATTTGATGAGTTTTTCTGGAGATGCTCTCAGTAGCCC
AGCACTCTCTGACCCAGCTCTTCTCCCACTCTACGGCCGCTGTATGCCAGCACGCCCTCATATTCAAT
GGCCTGTTCTCTCGGCTGCGAGACTTCTATGGGGAATCTGGTGGGGGTTGGATGACACCCTGGCGGATTT
CTGGGCACAGCTCCTGGAGAGAGTGTTCCTGCTGTGCACCCACAGTACAGCTTCCCCCTGACTACCTGC
TCTGCCTCTCAGCCTTGGCCTCATCTACCGATGGCTCTCTGCAGCCCTTTGGGGACTACCCCGCCGCCCTC
CGCCTGCAGATAACCCGACCCCTGGTGGCTGCCGAGCCTTTGTGCAGGGCCTGGAGACTGGAAGAAATGT
GGTCAGCGAAGCGCTTAAGGTTCCGGTGTCTGAAGGCTGCAGCCAGGCTCTGATGCGTCTCATCGGCTGTC
CCCTGTGCCGGGGGTCCCTCACTTATGCCCTGCCAGGGCTTCTGCCTCAACGTGGTTCGTGGCTGTCTC
AGCAGCAGGGGACTGGAGCCTGACTGGGGCAACTATCTGGATGGTCTCCTGATCCTGGCTGATAAGCTCCA
GGGCCCTTTTCTTTGAGCTGACGGCCGAGTCCATTGGGGTGAAGATCTCGGAGGGTTTGATGTACCTGC
AGGAAAACAGTGCGAAGGTGTCCGCCAGGTATTTACAGAGTGCGGCCCCCGACCCGGTGCTGCCCGC
AACCGTCGAGCCCCCGCCCCGGAAGAGCGGGCCCGCTGTGGTCGATGGTGACCGAGGAGGAGCGGCC
AACGACCGCCGAGGCACCAACCTGCACCCGGCTGGTGTGGGAGCTCCGCGAGCGTCTGGCCCGGATGCGGG
GCTTCTGGGCCCGGCTGTCCCTGACGGTGTGCGGAGACTCTCGCATGGCAGCGGACGCCTCGCTGGAGGCG
GCGCCCTGCTGGACCGGAGCCGGCGGGGCGGTACTTGCCGCCAGTGGTGGGGGCTCCCCGGCCGAGCA
GGTCAACAACCCGAGCTCAAGGTGGACGCTCGGGCCCCGATGTCCCGACACGGCGGGCTCGGCTACAGC
TCCGGGCGGCCACGGCCAGAATGAAAACGGCCGCACTGGGACACGACCTGGACGGGCAGGACGCAGATGAG
GATGCCAGCGGCTCTGGAGGGGACAGCAGTATGCAGATGACTGGATGGCTGGGGCTGTGGCTCCCCCAGC
CCGGCCTCCTCGGCTCCATACCTCCTAGAAGGGATGGTTCTGGGGGCAAAGGAGGAGGTGGCAGTGCCC
GCTACAACAGGGCCGGAGCAGGAGTGGGGGGCATCTATTGGTTTTACACCCAAACCATCTCATTTCTC
TCCCTCTCAGCCCTGGCCCTGCTTGGACCTCGATAACCGGGGAGGGGTGCCCTAGCATCAGAAGGTTTCAT
GGCCCTTTCC

The disclosed NOV8a nucleic acid sequence, localized to chromosome 7, has 1469 of 1785 bases (82%) identical to a *Rattus norvegicus* cerebroglycan mRNA (gb:GENBANK-ID:RATCRBGLVC|acc:L20468) ($E = 3.3e^{-261}$).

A disclosed NOV8a polypeptide (SEQ ID NO:20) encoded by SEQ ID NO:19 is 579 amino acid residues and is presented using the one-letter amino acid code in Table 8B. Signal P, Psort and/or Hydropathy results predict that NOV8a contains a signal peptide and is likely to be localized extracellularly with a certainty of 0.4467. The most likely cleavage site for a NOV8a peptide is between amino acids 23 and 24, at: GPG-SE.

Table 8B. Encoded NOV8a protein sequence (SEQ ID NO:20).

MSALRPLLLLLLPLCPGPGPGSEAKVTRSCAETRQVLGARGYSLNLIPPALISGEHLRVCPQEYTCSS ETEQRILIRETEATFRGLVEDSGSFLVHTLAARHRKFDEFLEMLSVAQHSLTQLFHSYGRLYAQHALIFN GLFSRLRDFYGESGEGLDLADFWAQLLERVFPLLHPQYSFPPDYLLCLSRASSTDGSLQPFQDPSRRL RLQITRTLVAARAFVQGLTGRNVVSEALKVPVSEGCSQALMRLIGCPLCRGVPVSLMPCQGFCLNVVRGCL SSRGLEPDWGNLYLDGLLILADKLQGPFSFELTAESIGVKISEGLMYLQENSAKVSAQVFQECGPPDPVPAR NRRAPPPREEAGRLWSMVTEERPTTAAGTNLHRLVWELRERLARMRGFWARLSLTVCDSRMAADASLEA APCWTGAGRGRLPPVVGGSAPAEQVNNPELKVDAAGPDVPTRRRLQLRAATARMKTAALGHDLGQDADE DASGGGGQYADDWMAGAVAPPARPPPPYPPRRDGGSGKGSGGSARYNQGRSRSGGASIGFHTQTILIL SLSALALLGPR
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The NOV8a amino acid sequence has 477 of 579 amino acid residues (82%) identical to, and 513 of 579 amino acid residues (88%) similar to, the *Rattus norvegicus* 579 amino acid residue glypican-2 precursor (cerebroglycan) protein (ptnr:SWISSPROT-ACC:P51653)($E = 1.1e^{-260}$).

NOV8a is expressed in at least the following tissues: Kidney, Spleen, Brain, Pediatric pre-B cell acute lymphoblastic leukemia. This information was derived by determining the tissue sources of the sequences that were included in the invention. SeqCalling sources: Kidney, Spleen, Brain; PublicEST sources: Pediatric pre-B cell acute lymphoblastic leukemia. In addition, NOV8a is predicted to be expressed in brain tissues because of the expression pattern of a closely related *Rattus norvegicus* cerebroglycan mRNA homolog (GENBANK-ID: gb:GENBANK-ID:RATCRBGLVC|acc:L20468).

NOV8b

A disclosed NOV8b nucleic acid of 1976 nucleotides (also referred to CG50970-02) encoding a novel Glypican-2 Precursor-like protein is shown in Table 8C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 54-56 and ending with a TAA codon at nucleotides 1449-1451. Putitive untranslated regions upstream from the initiation codon and downstream from the termination codon is underlined in Table 8C, and the start and stop codons are in bold letters.

The NOV8b amino acid sequence has 322 of 380 amino acid residues (84%) identical to, and 348 of 380 amino acid residues (91%) similar to, the *Rattus norvegicus* 579 amino acid residue glypican-2 precursor (cerebroglycan) protein (ptnr:SWISSPROT-ACC:P51653) ($E = 1.5e^{-210}$).

NOV8b is expressed in at least the following tissues: Aorta, Brain, Cartilage, Cervix, Liver, Lung, Oviduct/Uterine Tube/Fallopian tube, Parotid Salivary glands, Placenta, Prostate, Retina, Skeletal Muscle, Stomach, Temporal Lobe, Testis, Vein. This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

NOV8c

A disclosed NOV8c nucleic acid of 1613 nucleotides (also referred to CG50970-03) encoding a novel Glypican-2 Precursor-like protein is shown in Table 8E. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 1348-1350. A putitive untranslated region downstream from the termination codon is underlined in Table 8E, and the start and stop codons are in bold letters.

Table 8E. NOV8c Nucleotide Sequence (SEQ ID NO:23)

ATGTCCGCGCTGCGACCTCTCCTGCTTCTGCTGCTGCTCTGTGTCCCGGTCTGGTCCCGGAC
CCGGGAGCGAGGCAAAGGTACCCCGGAGTTGTGCAGAGACCCGGCAGGTGCTGGGGGCCCCGGG
ATATAGCTTAAACCTAATCCCTCCCGCCCTGATCTCAGGTGAGCACCTCCGGGTCTGTCCCCAG
GAGTACACCTGCTGTTCCAGTGAGACAGAGCAGAGGCTGATCAGGGAGACTGAGGCCACCTTCC
GAGGCCTGGTGGAGGACAGCGGCTCCTTTCTGGTTCACACACTGGCTGCCAGGCACAGAAATT
TGATGAGTTTTTCTGGAGATGCTCTCAGTAGCCAGCACTCTTGACCCAGCTCTTCTCCAC
TCCTACGGCCGCTGTATGCCAGCAGCCCTCATATTCAATGGCCTGTCTCTCGGCTGCGAG
ACTTCTATGGGAATCTGGTGAGGGGTTGGATGACACCCTGGCGGATTCTGGGCACAGCTCCT
GGAGAGAGTGTTCCTGCTGCTGCACCCACAGTACAGCTTCCCCCTGACTACCTGCTCTGCCTC
TCACGCTTGGCCTCATCTACCGATGGCTCTCTGCAGCCCTTGGGGACTCACCCCGCCGCTCC
GCCTGCAGATAACCCGGACCCCTGGTGGCTGCCCGAGCCTTTGTGCAGGGCCTGGAGACTGGAAG
AAATGTGGTCAGCGAAGCGCTTAAGGTGCCGGTGTCTGAAGGCTGCAGCCAGGCTCTGATGCGT
CTCATCGGCTGTCCCTGTGCCGGGGGTCCCTCACTTATGCCCTGCCAGGGCTTCTGCCTCA
ACGTGGTTTCGTGGCTGTCTCAGCAGCAGGGGACTGGAGCCTGACTGGGGCAACTATCTGGATGG
TCTCTGATCCTGGCTGATAAGCTCCAGGGCCCCCTTTCTTTGAGCTGACGGCCGAGTCCATT
GGGGTGAAGATCTCGGAGGGTTTGATGTACCTGCAGGAAAACAGTGCGAAGGTGTCCGCCAGG
TGTTTCAGGAGTGCGCCCCCCCCGACCCGGTGCCTGCCCGCAACCGTCGAGCCCCGCCGCCCG
GGAAGAGGCGGGCCGCTGTGGTTCGATGGTGACCGAGGAGGAGCGGCCACGACGGCCGAGGC
ACCAACCTGCACCGGCTGGTACTTGCCGCCAGTGGTGGGGGCTCCCCGGCCGAGCAGGTCAAC
AACCCGAGCTCAAGTGACGCTCGGGCCCCGATGTCCGACACGGCGGCTCGGCTACAGC
TCCGGGCGGCCACGGCCAGAATGAAAACGGCCGCACTGGGACACGACCTGGACGGGCAGGACGC
GGATGAGGATGCCAGCGGCTCTGGAGGGGACAGCAGTATGCAGATGACTGGATGGCTGGGGCT
GTGGCTCCCCCAGCCCGGCTCCTCGGCTCCATACCCTCCTAGAAGGGATGGTTCTGGGGGCA
AAGGAGGAGGTGGCAGTGCCGCTACAACAGGGCCGAGCAGGAGTGGGGGGCATCTATTGG
TTTTACACCCAAACCATCTCTCCTCTCAGACCTGGCCCTGCTTGGACCTCGATAA
CGGGGAGGGGTG

The disclosed NOV8c nucleic acid sequence, localized to chromosome 2, has 994 of 1172 bases (84%) identical to a *Rattus norvegicus* cerebroglycan mRNA (gb:GENBANK-ID:RATCRBGLVC|acc:L20468.1) ($E = 1.3e^{-237}$).

A disclosed NOV8c polypeptide (SEQ ID NO:24) encoded by SEQ ID NO:23 is 449 amino acid residues and is presented using the one-letter amino acid code in Table 8F. Signal P, Psort and/or Hydropathy results predict that NOV8c contains a signal peptide and is likely to be localized extracellularly with a certainty of 0.3700. The most likely cleavage site for a NOV8c peptide is between amino acids 23 and 24, at: GPG-SE.

Table 8F. Encoded NOV8c protein sequence (SEQ ID NO:24).

```
MSALRPLLLLLPLCPGPGPGSEAKVTRSCAETRQVLGARGYSNLIPPALISGEHLRVCPQEYTCSS
ETEQRLLIRETEATFRGLVEDSGSFLVHTLAARHRKFDEFFLEMLSVAQHSLTQLFSHSYGRLYAQHALIFN
GLFSRLRDFYGESGEGDDTLADFWAQLLERVFPLLHPQYSFPDPYLLCLSRLASSTDGSLQPPGDSRRL
RLQITRTLVAARAFVQGLETRNVVSEALKVPVSEGCSQALMRLIGCPLCRGVPSLMPQQGFCNLNVVRGCL
SSRGLEPDWGNLYLDGLLILADKLQGPFSFELTAESIGVKISEGLMYLQENSAKVSQVFQECGPPDPVPA
NRRAPPPREEAGRLWSMVTEERPTTAAGTNLHRLVLAASGRGLPGRAGQQPRAQGGRLGPRCPDTAASAT
APGGHCQNGRTGTRPGRARG
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The NOV8c amino acid sequence has 334 of 391 amino acid residues (85%) identical to, and 359 of 391 amino acid residues (91%) similar to, the *Rattus norvegicus* 579 amino acid residue glypican-2 precursor (cerebroglycan) protein (ptnr:SWISSPROT-ACC:P51653) ($E = 1.4e^{-183}$).

NOV8c is expressed in at least the following tissues: Aorta, Brain, Cartilage, Cervix, Liver, Lung, Oviduct/Uterine Tube/Fallopian tube, Parotid Salivary glands, Placenta, Prostate, Retina, Skeletal Muscle, Stomach, Temporal Lobe, Testis, Vein. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the NOV8c sequence.

NOV8d

A disclosed NOV8d nucleic acid of 725 nucleotides (also referred to CG50970-04) encoding a novel Glypican-2 Precursor-like protein is shown in Table 8G. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 160-162 and ending with a TAA codon at nucleotides 688-690. Putitive untranslated regions upstream from the initiation codon and downstream from the termination codon is underlined in Table 8G, and the start and stop codons are in bold letters.

Table 8G. NOV8d Nucleotide Sequence (SEQ ID NO:25)

```
CGCCTGGTCCAGCTATCGTGCTCGGTATTTCAGTTTTCCGGAGCAGCGCTCTTTCTCTGGCCCGC
GGAACGGTCCCGCGGCCGAGTACCGGATTCGCGAGTTTGGGAGGCTCTGCTTTCTCCTTAGGA
CCCACTTTGCCGTCTGGGGTGGCTGCAGTTATGTCCGCGCTGCGACCTCTCCTGCTTCTGCTG
CTGCCTCTGTGTCCCGGTCTGGTCCCGGACCGGGAGCGAGGCAAAGGTACCCGGAGTTGTG
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CAGAGACCCGCGAGGTGCTGGGGGCCCGGGGATATAGCTTAAACCTAATCCCTCCCGCCCTGAT
 CTCAGGTGAGCACCTCCGGGTCTGTCCCCAGGAGTACACCTGCTGTTCCAGTGAGACAGAGCAG
 AGGCTGATCAGGGAGACTGAGGCCACCTTCCGAGGCCTGGTGGAGGACAGCGGCTCCTTTCTGG
 TTCACACACTGGCTGCCAGGCACAGAAAATTTGATGAGTTTTTCTGGAGATGCTCTCAGTAGC
 CCGGCCTCCTCGGCCTCCATACCCTCCTAGAAGGATGGTTCTGGGGGCAAAGGAGGAGGTGGC
 AGTCCCCGCTACAACCAGGGCCGAGCAGGAGTGGGGGGCATCTATTGGTTTTACACCCAAA
 CCATCCTCATTCTCTCCCTCTCAGCCCTGGCCTTGCTTGGACCTCGATAACGGGGGAGGGGTGC
 CCTAGCATCAGAAGGGTTCAT

The disclosed NOV8d nucleic acid sequence, localized to chromosome 2, has 448 of 545 bases (82%) identical to a *Rattus norvegicus* cerebroglycan mRNA (gb:GENBANK-ID:RATCRBGLVC|acc:L20468.1) ($E = 4.2e^{-101}$).

A disclosed NOV8d polypeptide (SEQ ID NO:26) encoded by SEQ ID NO:25 is 176 amino acid residues and is presented using the one-letter amino acid code in Table 8H. Signal P, Psort and/or Hydropathy results predict that NOV8d contains a signal peptide and is likely to be localized extracellularly with a certainty of 0.4467. The most likely cleavage site for a NOV8d peptide is between amino acids 23 and 24, at: GPG-SE.

Table 8H. Encoded NOV8d protein sequence (SEQ ID NO:26).

MSALRPLLLLLLPLCPGPGPGSEAKVTRSCAETRQVLGARGYSLNLIIPPALISGEHLRVCPQEYTCSS
 ETEQRLIRETEATFRGLVEDSGSFLVHTLAARHRKFDEFFLEMLSVARPPRPYPYPPRRDGGSGKGKGGGSAR
 YNQRSRSGGASIGFHTQTILILSLALALLGPR

The NOV8d amino acid sequence has 103 of 119 amino acid residues (86%) identical to, and 114 of 119 amino acid residues (95%) similar to, the *Rattus norvegicus* 579 amino acid residue glypican-2 precursor (cerebroglycan) protein (ptnr:SWISSPROT-ACC:P51653) ($E = 2.6e^{-73}$).

NOV8d is expressed in at least the following tissues: Aorta, Brain, Cartilage, Cervix, Liver, Lung, Oviduct/Uterine Tube/Fallopian tube, Parotid Salivary glands, Placenta, Prostate, Retina, Skeletal Muscle, Stomach, Temporal Lobe, Testis and Vein. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the NOV8d sequence.

Possible SNPs found for GPCR8d are listed in Table 8I.

Table 8I: SNPs			
Consensus Position	Depth	Base Change	PAF
227	19	T > C	0.105
482	55	C > T	0.036
523	55	A > G	0.036
548	55	G > A	0.036
573	53	G > A	0.038

684	28	T > C	0.393
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The NOV8a - NOV8d proteins are very closely homologous as shown in the alignment in Table 8J.

Table 8J Alignment of NOV8a – NOV8d

	10	20	30	40
NOV8A	MSALRPLLLLLPLCPGPGPGSEAKVTRSCAETQVLG			
NOV8B	MSALRPLLLLLPLCPGPGPGSEAKVTRSCAETQVLG			
NOV8C	MSALRPLLLLLPLCPGPGPGSEAKVTRSCAETQVLG			
NOV8D	MSALRPLLLLLPLCPGPGPGSEAKVTRSCAETQVLG			
	50	60	70	80
NOV8A	ARGYSNLIPPALISGEHLRVCPQEYTCSSSETEQRLIRE			
NOV8B	ARGYSNLIPPALISGEHLRVCPQEYTCSSSETEQRLIRE			
NOV8C	ARGYSNLIPPALISGEHLRVCPQEYTCSSSETEQRLIRE			
NOV8D	ARGYSNLIPPALISGEHLRVCPQEYTCSSSETEQRLIRE			
	90	100	110	120
NOV8A	TEATFRGLVEDSGSFLVHTLAARHRKFDEFFLEMLSVAQH			
NOV8B	TEATFRGLVEDSGSFLVHTLAARHRKFDEFFLEMLSVAQH			
NOV8C	TEATFRGLVEDSGSFLVHTLAARHRKFDEFFLEMLSVAQH			
NOV8D	TEATFRGLVEDSGSFLVHTLAARHRKFDEFFLEMLSVA--			
	130	140	150	160
NOV8A	SLTQLFSHSYGRLYAQHALIFNGLFSRLRDFYGESGEGLD			
NOV8B	SLTQLFSHSYGRLYAQHALIFNGLFSRLRDFYGESGEGLD			
NOV8C	SLTQLFSHSYGRLYAQHALIFNGLFSRLRDFYGESGEGLD			
NOV8D				
	170	180	190	200
NOV8A	DTLADEFWAQLLERVFPILLEPQYSFPPDYLLCLSRLASSTD			
NOV8B	DTLADEFWAQLLERVFPILLEPQYSFPPDYLLCLSRLASSTD			
NOV8C	DTLADEFWAQLLERVFPILLEPQYSFPPDYLLCLSRLASSTD			
NOV8D				
	210	220	230	240
NOV8A	GSLQPFGDSPRRLRLQITRTLVAARAFVQGLTGRNVVSE			
NOV8B	GSLQPFGDSPRRLRLQITRTLVAARAFVQGLTGRNVVSE			
NOV8C	GSLQPFGDSPRRLRLQITRTLVAARAFVQGLTGRNVVSE			
NOV8D				
	250	260	270	280
NOV8A	ALKVPVSEGCQSALMRLIGCPLCRGVPSLMP CQGFCNLVV			
NOV8B	ALKVPVSEGCQSALMRLIGCPLCRGVPSLMP CQGFCNLVV			
NOV8C	ALKVPVSEGCQSALMRLIGCPLCRGVPSLMP CQGFCNLVV			
NOV8D				
	290	300	310	320
NOV8A	RGCLSSRGLEPDWGNLYLDGLLILADKLQGPFSFELTAESI			
NOV8B	RGCLSSRGLEPDWGNLYLDGLLILADKLQGPFSFELTAESI			
NOV8C	RGCLSSRGLEPDWGNLYLDGLLILADKLQGPFSFELTAESI			
NOV8D				
	330	340	350	360
NOV8A	GVKISEGLMYLQENS AKVSAQVFQECGPPDPV PARNRRAP			
NOV8B	GVKISEGLMYLQENS AKVSAQVFQECGPPDPV PARNRRAP			

gi 7106325 ref NP_035951.1	glypican 6 [Mus musculus]	555	226/512 (44%)	332/512 (64%)	1e-124
gi 5031719 ref NP_05699.1	glypican 6 precursor [Homo sapiens]	555	225/512 (43%)	330/512 (63%)	1e-122
gi 6680059 ref NP_032176.1	glypican 4 [Mus musculus]	557	208/487 (42%)	314/487 (63%)	1e-114
gi 13879296 gb AAH06622.1 AAH06622 (BC006622)	glypican 4 [Mus musculus]	557	208/487 (42%)	314/487 (63%)	1e-114

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 8L.

Table 8L. ClustalW Analysis of NOV8a

- 1) Novel NOV8a (SEQ ID NO:20)
- 2) gi|1708021|sp|P51653|GPC2_RAT glypican-2 precursor (cerebroglycan) (HSPG M13) [Rattus norvegicus] (SEQ ID NO:70)
- 3) gi|7106325|ref|NP_035951.1| glypican 6 [Mus musculus] (SEQ ID NO:71)
- 4) gi|5031719|ref|NP_005699.1| glypican 6 precursor [Homo sapiens] (SEQ ID NO:72)
- 5) gi|6680059|ref|NP_032176.1| glypican 4 [Mus musculus] (SEQ ID NO:73)
- 6) gi|13879296|gb|AAH06622.1|AAH06622 (BC006622) glypican 4 [Mus musculus] (SEQ ID NO:74)

NOV8a	1	MSALRPILLLLPLCPGPGPGGSEAKVTRSCAETROVLGARGYSLNLI PPAISGEHLR	60
gi 1708021	1	MSAVRPILLLLPLCPGPGPGHGSEAKVVRSCAETROVLGARGYSLNLI PPSLISGEHLQ	60
gi 7106325	1	--MPSWIRAVILPLSGLLLTLFAAADVKARSCSEVRQAYGAKGFSLADIPYQETAGEHLR	58
gi 5031719	1	--MPSWIGAVILPLGLLLSLPAGADVKAARSCSEVRQAYGAKGFSLADIPYQETAGEHLR	58
gi 6680059	1	--MARLGLIALLLCTLAALSASLLAELKSKSCSEVRRLYVSKGFNKNDAPLYEINGDHLK	58
gi 13879296	1	--MARLGLIALLLCTLAALSASLLAELKSKSCSEVRRLYVSKGFNKNDAPLYEINGDHLK	58
NOV8a	61	VCPQEYTCSSSETEORLIRETEATERGLVEDSGSFLVHTLAARHKKFDEFFLEMLSVAQH	120
gi 1708021	61	ICPQEYTCSSSETEOKLIRDAEVTFRGLVEDSGSFLIHTLAARHKKFDEFFREMLSISQH	120
gi 7106325	59	ICPQEYTCCTTEMDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENA EK	118
gi 5031719	59	ICPQEYTCCTTEMDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENA EK	118
gi 6680059	59	ICPQDYTCSSQEMBEKYSLSQSKDDFKTVVSEQNHLOAIFASRYKKFDEFFKELLENA EK	118
gi 13879296	59	ICPQDYTCSSQEMBEKYSLSQSKDDFKTVVSEQNHLOAIFASRYKKFDEFFKELLENA EK	118
NOV8a	121	SLTQLFSHSYGRLYAOHALIENGLFSRLRDFYGESGEGDDTLADFWAQLLERVFPILLHP	180
gi 1708021	121	SLAQLFSHSYGRLYSOHAVIENSLSGLRDYVEKSGEGDDTLADFWAQLLERAFPIILLHP	180
gi 7106325	119	SLNDMFVRTYGMLYMONSEVFODLFTLKYRYTGGNVNLEEMNDFWARLLERMFOQLINP	178
gi 5031719	119	SLNDMFVRTYGMLYMONSEVFODLFTLKYRYTGGNVNLEEMNDFWARLLERMFOQLINP	178
gi 6680059	119	SLNDMFVKTYGCHLYMONSELKDLLEVELKRYVYAGNVNLEEMNDFWARLLERMFRVNS	178
gi 13879296	119	SLNDMFVKTYGCHLYMONSELKDLLEVELKRYVYAGNVNLEEMNDFWARLLERMFRVNS	178
NOV8a	181	QYSFPDPDYLLCLSLASSTDGSLOPFGSPRRRLQITRTLVAARAFVQGLTGRNVVSE	240
gi 1708021	181	QYSFPDPDELCLTRLTSTADGSLPFGSPRRRLQITRALVAARALVQGLTGRNVVSE	240
gi 7106325	179	QYHFSEDYLECYSKYT----DCLKPFGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANR	234
gi 5031719	179	QYHFSEDYLECYSKYT----DCLKPFGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANR	234
gi 6680059	179	QYHFTDYLECYSKYT----ECLKPFGDVPRKLKIQVTRAFVAARTFAOGLAVARDVVSK	234
gi 13879296	179	QYHFTDYLECYSKYT----ECLKPFGDVPRKLKIQVTRAFVAARTFAOGLAVARDVVSK	234
NOV8a	241	ALKVPVSEGGSCALMRLICPLCRGVPSLMPGQGFCLNVVRGCLSSRG-LEPDWGNLYDG	299
gi 1708021	241	ALKVPMLEGGRCALMRLICPLCRGVPSLMPGQGFCLNVVHAGCLSSRG-LEPDWGGYLDG	299
gi 7106325	235	VSKVSPTPGCCIRALMKMLYCPYCRGLETVRPONNYCLNVMGCLANQADLDTEWNLFIDA	294
gi 5031719	235	VSKVSPTPGCCIRALMKMLYCPYCRGLETVRPONNYCLNVMGCLANQADLDTEWNLFIDA	294
gi 6680059	235	VSVVNPTAQCTHALKMLIYCSHCRGLVTVKPCYNYCSNIMRGCLANQCDLDFEWNNEIDA	294
gi 13879296	235	VSVVNPTAQCTHALKMLIYCSHCRGLVTVKPCYNYCSNIMRGCLANQCDLDFEWNNEIDA	294
NOV8a	300	LLILADKLOGPFSFELTAESIGVKISEGLMYLQENSANVSAQVFCBCCGPFDPVARNRRA	359
gi 1708021	300	LLLLAEKLOGPFSFELAAESIGVKISEGLMHLQENSANVSAQVFCBCCGPHPVQSRNRRRA	359
gi 7106325	295	MLLVAERLEGPPNIESVMDPIDVKISDAIMNMQNSMCQVSAKVFCQCCGPKPAPALRSAR	354
gi 5031719	295	MLLVAERLEGPPNIESVMDPIDVKISDAIMNMQNSMCQVSAKVFCQCCGPKPAPALRSAR	354
gi 6680059	295	MLMVAERLEGPPNIESVMDPIDVKISDAIMNMQNSVQVSAKVFCQCCGPKPLPAGRISR	354
gi 13879296	295	MLMVAERLEGPPNIESVMDPIDVKISDAIMNMQNSVQVSAKVFCQCCGPKPLPAGRISR	354
NOV8a	360	PPFREEAGRLWSMVTBEERPTTAAGTNLHRLVWELRERIRARMGFNARLSITVCGDSRMA	419
gi 1708021	360	PAPREETSRSRSSABEERPTTAAGTNLHRLVWELRERISRVRGFNAGLPVITVCGDSRMA	419
gi 7106325	355	SAPEN-FNTRFRPNPEERPTTAAGTS-DRLVTDIKEKIKLSKKVNSALPYTIKDERVT	413

gi 5031719	355	SASEN-FNTRFRPYNPEERPTTAAGTSLDRLVTDVKEKLSKKVWSALPYTICKDESVT	413
gi 6680059	355	SISESAFSARFRPYHPEORPTTAAGTSLDRLVTDVKEKLSKKVWSALPYTICKDESVT	414
gi 13879296	355	SISESAFSARFRPYHPEORPTTAAGTSLDRLVTDVKEKLSKKVWSALPYTICKDESVT	414
NOV8A	420	ADASLEAAPCWTGAGRGYLPVVGGSAPAEVNNPELKVDASGPDVPTRRRLQLRAATA	479
gi 1708021	420	ADLSQBAAPCWTGVGRGRYMSFVVVGSLSNEQLHN--PELDTSSPDVPTRRRLHLRAATA	477
gi 7106325	414	AGTSNBEE-CWNGHSAKARYLPEIMNDGLTNOINN-----	446
gi 5031719	414	AGTSNBEE-CWNGHSAKARYLPEIMNDGLTNOINN-----	446
gi 6680059	415	AGNENDD-CWNGKGSRYLFAVTGNGLANOGNN-----	447
gi 13879296	415	AGNENDD-CWNGKGSRYLFAVTGNGLANOGNN-----	447
NOV8A	480	RMKTAALGHDLGDQDAEDASGSGGQQYADDWMA--GAVAPPARPPRPYPYPRRGGSGG	537
gi 1708021	478	RMKAAALGQDLDMDHDAEDASGSGGQQYADDWKAGAAPVPPARPPRPYPRRGGGLGV	537
gi 7106325	446	-----PEVEVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDE	491
gi 5031719	446	-----PEVEVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDE	491
gi 6680059	447	-----PEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDTSDE	492
gi 13879296	447	-----PEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDTSDE	492
NOV8A	538	KCGGGS-----ARYNQGRSRSGGASIGFHTQTILILSLSAALG	577
gi 1708021	538	RGGSGS-----ARYNQGRSRNLGSSVGLHAPRVFILLPSALTULG	577
gi 7106325	492	SSCGSGSGCMDDVCPTFEFVTEAPAVDP-DRREESSASKFSSSLISWSLVCMLAL	550
gi 5031719	492	SSCGSGSGCMDDVCPTFEFVTEAPAVDP-DRREVDSAAQRGHSLSWSLTCIVLAL	550
gi 6680059	493	SSCEGSGSGCEYQQCPSEFEYNATDHSKGSANEKADSAGGAHAETKPYLLAALCILFLAV	552
gi 13879296	493	SSCEGSGSGCEYQQCPSEFEYNATDHSKGSANEKADSAGGAHAETKPYLLAALCILFLAV	552
NOV8A	578	PR--- 579	
gi 1708021	578	LR--- 579	
gi 7106325	551	QLYR 555	
gi 5031719	551	QLCR 555	
gi 6680059	553	QGEWR 557	
gi 13879296	553	QGEWR 557	

Table 8M lists the domain description from DOMAIN analysis results against NOV8a. This indicates that the NOV8a sequence has properties similar to those of other proteins known to contain these domains.

Table 8M. Domain Analysis of NOV8a

gnl|Pfam|pfam01153, Glypican. (SEQ ID NO:98)
Length = 554 residues, 86.1% aligned
Score = 536 bits (1380), Expect = 2e-153

NOV8a	24	SEAKVTRSCAETRQVLGARGYSNLNIPPALISGEHLRVCPQEYTCSSSETEQRLIRETEA	83
01153	17	AEGSKSRSCAEVRQLFGAKGFSLNDVPQSEISGEHLQICPQGYTCSSSEMEEKLQLKARG	76
NOV8a	84	TFRGLVEDSGSFLVHTLAARHRKFEFFLEMLSVAQHSLTQLFSHSYGRLYAQHALIFNG	143
01153	77	DFEQLLQDSSSLQFLLATNAKKFQEHFEELNISENYLNALFSKTYGRLYPQNAEMFKD	136
NOV8a	144	LFSRLRDFYGESGEGLDDTLADFWAQLLERVFLLHPQYSFPDPYLLCLSRLASSTDGSL	203
01153	137	LFTELRLYRGSNINLEALNEFWARLLERAFKQLHGQYDSDPDYLECLRKARE---DL	192
NOV8a	204	QPFGDSPPRLRLQITRTLVAARAFVQGLETRNVVSEALKVPVSEGCSQALMRLIGCPLC	263
01153	193	KPFGDIPRRLMLQVTRALVAARTFLQGLNVGIEVVSVKVDQVPLSKECSRALLKMIYCPHC	252
NOV8a	264	RGVPSLMPCQGFCLNVVRGCLSSRG-LEPDWGNLYDGLLILADKLQGPFSFELTAESIGV	322
01153	253	RGLPSVKPCYGYCLNVMRGCLANQADLDPEWRYIDSLELLADKMLGPYDIENVILSIHT	312
NOV8a	323	KISEGLMYLQENSAKVAQVFQECPPDPVPARNRRAPPPREEAGRLWSMVTEERPTTA	382
01153	313	KISEAIMALQENGVKLTAKVFQCGG---TPKPTPYGSASGPDKRSKRPLKPEERPTTE	368

Hyperproglucagonemia, Bethlem myopathy, Brachydactyly type E, Brachydactyly-mental retardation syndrome, Finnish lethal neonatal metabolic syndrome, susceptibility to 2, Simpson-Golabi-Behmel syndrome, type 1 and type 2 and Beckwith-Wiedemann syndrome. The NOV8 nucleic acid encoding Glypican-2 Precursor-like protein, and the Glypican-2 Precursor-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV9

A disclosed NOV9 nucleic acid of 985 nucleotides (also referred to AC011005_da2/139943578) encoding a novel Mitogen Activated Protein Kinase Kinase 2-like protein is shown in Table 9A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 54-56 and ending with a TGA codon at nucleotides 975-977. The start and stop codons are in bold letters.

Table 9A. NOV9 Nucleotide Sequence (SEQ ID NO:27)

TCCACTACGGGCCAGGCTAGAGGCGCCGCGCCGCGCGGCCCGCGGAGCCCCGATGCTGGCCCGGAGGAAG
CCGGTGTGCGCGGCTCACCATCAACCCATACCATCGCCGAGGGCCATCCCTACCAGCGAGGGCGCCTC
CGAGGCAAACCTGGTGGACCTGCAGAAGAAGCTGGAGGAGCTGGAACCTGACGAGCAGCAGAAGAAGCGGC
TGGAAGCCTTTCTACCCAGAAAGCCAAGGTCGGCGAACTCAAAGACGATGACTTCGAAAGGATCTCAGAG
CTGGGCGCGGCAACGGCGGGTGGTCACCAAAGTCCAGCACAGACCCTCGGGCCTCATCATGGCCAGGAA
GCTGATCCACCTTGAGATCAAGCCGGCCATCCGGAACGATCATCCGCGAGCTGCAGGTCCTGCCAGAA
GCAACTCGCCGTACATCGTGGGCTTCTACGGGGCTTCTACAGTGACGGGAGATCAGCATTTGCATGGAA
CACATGGACGGCGGCTCCCTGGACAGGTGCTGAAAGAGGCCAAGAGGATTCCCGAGGAGATCCTGGGAA
AGTCAGCATCGCGGTTCTCCGGGGCTTGGCGTACCTCCGAGAGAAGCACCAGATCATGCACCGAGATGTGA
AGCCCTCCAACATCCTCGTGAACCTTAGAGGGGAGATCAAGCTGTGTGACTTCGGGGTGAGCGGCCAGCTC
ATCGACTCCATGGCAACTCCTTCGTGGGCACGCGCTCTACATGGCTCCACCTCCTAAGCTGCCCAACGG
TGTGTTCACCCCGACTTCCAGGAGTTTGTCAATAAATGCCTCATCAAGAACCAGCGGAGCGGGCGGACC
TGAAGATGCTCACAACCACACCTTCATCAAGCGGTCGAGGTGGAAGAAGTGATTTGCGCGCTGGTTG
TGTA AACCTGCGGCTGAACAGCCCGGCACACCCAGCGCACC GCGCTGTGACAGTGGCAA

The disclosed NOV9 nucleic acid sequence has 754 of 759 bases (99%) identical to a *Homo sapiens* ERK activator kinase (MEK2) mRNA from (gb:GENBANK-ID:HUMMEK2NF|acc:L11285) ($E = 1.3e^{-211}$). The NOV9 nucleic acid sequence contains numerous SNPs which result in various amino acid changes.

A disclosed NOV9 polypeptide (SEQ ID NO:28) encoded by SEQ ID NO:27 is 307 amino acid residues and is presented using the one-letter amino acid code in Table 9B. Signal P, Psort and/or Hydropathy results predict that NOV9 does not contain a signal peptide and is likely to be localized in the cytoplasm with a certainty of 0.5500.

Table 9B. Encoded NOV9 protein sequence (SEQ ID NO:28).

MLARRKPVLPALTINPTIAEGPSPTSEGASEANLVDLQKKLEELDEQQKKRLEAFLTQKAKVGELKDD
FERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGA
FYS DGE
ISICMEHMDGGS LDQVLKEAKRIPEEILGKVSIAVLRGLAYLREKHQIMHRDVKPSNILVNSRGEIKL
CDF
GVSGQLIDSMANSFVGTRSYMAPFPKLPNGVFTPDFQEFVNKCLIKNPAERADLKMLTNHTFIK
RSEVEEV

The NOV9 amino acid sequence has 236 of 236 amino acid residues (100%) identical to, and 236 of 236 amino acid residues (100%) similar to, the *Homo sapiens* 400 amino acid residue mitogen-activated protein kinase kinase 2 (EC 2.7.1.-) (Map kinase kinase 2)

5 (MAPKK 2) (ERK activator kinase 2 (ptnr:SWISSPROT-ACC:P36507) ($E = 8.2e^{-161}$).

NOV9 is expressed in at least the following tissues: Adrenal Gland/Suprarenal gland, Amygdala, Bone, Bone Marrow, Brain, Colon, Coronary Artery, Dermis, Epidermis, Foreskin, Heart, Hypothalamus, Kidney, Liver, Lung, Lymph node, Lymphoid tissue, Mammary gland/Breast, Muscle, Nervous, Ovary, Pancreas, Peripheral Blood, Pituitary Gland, Placenta, Prostate, Retina, Small Intestine, Spleen, Stomach, Testis, Thymus, Tongue, Tonsils, Tumor, Umbilical Vein, Uterus, Whole Organism. This information was derived by determining the tissue sources of the sequences that were included in the invention. In addition, NOV9 is predicted to be expressed in the following tissues because of the expression pattern of a closely related *Homo sapiens* ERK activator kinase (MEK2) mRNA homolog (GENBANK-
15 ID: gb:GENBANK-ID:HUMMEK2NF|acc:L11285): Lymphoid tissue, Nervous tissue, Gastrointestinal tissue, Peripheral Blood, and Cardiovascular tissue.

NOV9 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 9C.

Table 9C. BLAST results for NOV9

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13651323 ref XP_016871.1	similar to mitogen-activated protein kinase kinase 2; protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2) [Homo sapiens]	325	236/236 (100%)	236/236 (100%)	1e-133
gi 13489054 ref NP_109587.1	mitogen-activated protein kinase kinase 2; protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2) [Homo sapiens]	400	236/236 (100%)	236/236 (100%)	1e-131
gi 1096928 prf 2113192A	MEK2 protein [Rattus norvegicus]	400	229/236 (97%)	235/236 (99%)	1e-129
gi 12844163 dbj BAB26261.1 (AK009392)	putative [Mus musculus]	401	229/236 (97%)	235/236 (99%)	1e-129
gi 15990388 gb AAH14830.1 AAH14830 (BC014830)	Unknown (protein for MGC:25475) [Mus musculus]	401	229/236 (97%)	235/236 (99%)	1e-129

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 9D.

Table 9D Information for the ClustalW proteins

- 1) NOV9 (SEQ ID NO:28)
- 2) [gi|13651323 ref|XP_016871.1](#) similar to mitogen-activated protein kinase kinase 2; protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2) [Homo sapiens] (SEQ ID NO:75)
- 3) [gi|13489054 ref|NP_109587.1](#) mitogen-activated protein kinase kinase 2; protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2) [Homo sapiens] (SEQ ID NO:76)
- 4) [gi|1096928|prf|2113192A](#) MEK2 protein [Rattus norvegicus] (SEQ ID NO:77)
- 5) [gi|12844163|dbj|BAB26261.1](#) (AK009392) putative [Mus musculus] (SEQ ID NO:78)
- 6) [gi|15990388 gb|AAH14830.1|AAH14830](#) (BC014830) Unknown (protein for MGC:25475) [Mus musculus] (SEQ ID NO:79)

NOV9	1	MLARRKPVLPALTINPTIAEGSPSTSEGASEANLVDLQKKLEELDLDEQQRKLEAFLTQ	60
gi 13651323	1	MLARRKPVLPALTINPTIAEGSPSTSEGASEANLVDLQKKLEELDLDEQQRKLEAFLTQ	60
gi 13489054	1	MLARRKPVLPALTINPTIAEGSPSTSEGASEANLVDLQKKLEELDLDEQQRKLEAFLTQ	60
gi 1096928	1	MLARRKPVLPALTINPTIAEGSPSTSEGASEANLVDLQKKLEELDLDEQQRKLEAFLTQ	60
gi 12844163	1	MLARRKPVLPALTINPTIAEGSPSTSEGASEANLVDLQKKLEELDLDEQQRKLEAFLTQ	60
gi 15990388	1	MLARRKPVLPALTINPTIAEGSPSTSEGASEANLVDLQKKLEELDLDEQQRKLEAFLTQ	60
NOV9	61	KAKVGELKDDDFERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQ	120
gi 13651323	61	KAKVGELKDDDFERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQ	120
gi 13489054	61	KAKVGELKDDDFERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQ	120
gi 1096928	61	KAKVGELKDDDFERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQ	120
gi 12844163	61	KAKVGELKDDDFERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQ	120
gi 15990388	61	KAKVGELKDDDFERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQ	120
NOV9	121	VLHECNSPYIVGFYGFYSDGEISICMEHMDGGSLDQVLKEAKRIPEDILGKVSIAVLRG	180
gi 13651323	121	VLHECNSPYIVGFYGFYSDGEISICMEHMDGGSLDQVLKEAKRIPEDILGKVSIAVLRG	180
gi 13489054	121	VLHECNSPYIVGFYGFYSDGEISICMEHMDGGSLDQVLKEAKRIPEDILGKVSIAVLRG	180
gi 1096928	121	VLHECNSPYIVGFYGFYSDGEISICMEHMDGGSLDQVLKEAKRIPEDILGKVSIAVLRG	180
gi 12844163	121	VLHECNSPYIVGFYGFYSDGEISICMEHMDGGSLDQVLKEAKRIPEDILGKVSIAVLRG	180
gi 15990388	121	VLHECNSPYIVGFYGFYSDGEISICMEHMDGGSLDQVLKEAKRIPEDILGKVSIAVLRG	180
NOV9	181	LAYLREKHQIMHRDVKPSNILVNSRGEIKLDFGVSGQLIDSMANSFVGTRSYMA-----	235
gi 13651323	181	LAYLREKHQIMHRDVKPSNILVNSRGEIKLDFGVSGQLIDSMANSFVGTRSYMA-----	240
gi 13489054	181	LAYLREKHQIMHRDVKPSNILVNSRGEIKLDFGVSGQLIDSMANSFVGTRSYMA-----	240
gi 1096928	181	LAYLREKHQIMHRDVKPSNILVNSRGEIKLDFGVSGQLIDSMANSFVGTRSYMSPERLQ	240
gi 12844163	181	LAYLREKHQIMHRDVKPSNILVNSRGEIKLDFGVSGQLIDSMANSFVGTRSYMSPERLQ	240
gi 15990388	181	LAYLREKHQIMHRDVKPSNILVNSRGEIKLDFGVSGQLIDSMANSFVGTRSYMSPERLQ	240
NOV9	235	-----	235
gi 13651323	241	GTHYSVQSDIWSMGLSLVELAIGRYPIPPDAKELEAIFGRPVVDCADGEPHSVSPRPRP	300
gi 13489054	241	GTHYSVQSDIWSMGLSLVELAIGRYPIPPDAKELEAIFGRPVVDCADGEPHSVSPRPRP	300
gi 1096928	241	GTHYSVQSDIWSMGLSLVELAIGRYPIPPDAKELEAIFGRPVVDCADGEPHSVSPRPRP	300
gi 12844163	241	GTHYSVQSDIWSMGLSLVELAIGRYPIPPDAKELEAIFGRPVVDCADGEPHSVSPRPRP	300
gi 15990388	241	GTHYSVQSDIWSMGLSLVELAIGRYPIPPDAKELEAIFGRPVVDCADGEPHSVSPRPRP	300
NOV9	235	-----PPPKLPNG---VETPDPQEFVNKCLIKNPAAE	263
gi 13651323	254	-----LSLVELAVGRYPPIPPDAKELE--AIFGRPVV	284
gi 13489054	301	PGRPIIS-GHGMDSRPAMAFELLDYIVNEPPPKLPNG---VETPDPQEFVNKCLIKNPAAE	356
gi 1096928	301	PGRPIIS-GHGMDSRPAMAFELLDYIVNEPPPKLPNG---VETPDPQEFVNKCLIKNPAAE	356
gi 12844163	301	PGRPIIS-GHGMDSRPAMAFELLDYIVNEPPPKLPNG---VETPDPQEFVNKCLIKNPAAE	357
gi 15990388	301	PGRPIIS-GHGMDSRPAMAFELLDYIVNEPPPKLPNG---VETPDPQEFVNKCLIKNPAAE	356
NOV9	264	RADLKMLTNHTFIKRSEVEEVDFAGWLQRTLRLLKQPSTPTTRTAV	307
gi 13651323	285	DGEEGEPHSISPRIRPPCRPVSVTGWLAG---LPWPSSLNSWIL	325
gi 13489054	357	RADLKMLTNHTFIKRSEVEEVDFAGWLQRTLRLLKQPSTPTTRTAV	400
gi 1096928	357	RADLKMLTNHTFIKRSEVEEVDFAGWLQRTLRLLKQPSTPTTRTAV	400
gi 12844163	358	RADLKMLTNHTFIKRSEVEEVDFAGWLQRTLRLLKQPSTPTTRTAV	401
gi 15990388	357	RADLKMLTNHTFIKRSEVEEVDFAGWLQRTLRLLKQPSTPTTRTAV	400

Tables 9E and 9F list the domain description from DOMAIN analysis results against NOV9. This indicates that the NOV9 sequence has properties similar to those of other proteins known to contain these domains.

Table 9E. Domain Analysis of NOV9

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily. (SEQ ID NO:99)
Length = 256 residues, 100.0% aligned
Score = 184 bits (468), Expect = 5e-48

NOV9	72	FERISELGAGNGGVVTKVQHRPSGLIMARKLIHLE-IKPAIRNQIIRELQVLHECNSPYI	130
		+ + + + + ++ + + + +++ + +	
00220	1	YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKRERILREIKILKKLDHPNI	60
NOV9	131	VGFGAFYSDGEISICMEHMDGGSGLDQVLKEAKRIPEEILGKVSIAVLRGLAYLREKHQI	190
		++ + + + + + + + + +	
00220	61	VKLYDVFEDDDKLYLVMYCEGGDLFDLLKKRGRLEDEARFYARQILSALEYL-HSQGI	119
NOV9	191	MHRDVKPSNILVNSRGEIKLCDFGVSGQLIDS--MANSFVGTRSYMAP-----	236
		+ + ++ + ++ + +	
00220	120	IHRDLKPENILLSDSGHVKLADFLAKQLDSGGTLLTTFVGTPEYMAPEVLLGKGYGKAV	179
NOV9	237	-----PPKLPNGVFTPDFQEFVNKCLIK	259
		+ + + + +	
00220	180	DIWSLGVILYELLTGKPPFPDQLLALFKKIGKPPPPPPPEWKISPEAKDLIKKLLVK	239
NOV9	260	NPAERADLKMLTNHTFI	276
		+ + +	
00220	240	DPEKRLTAEAELEHPFF	256

Table 9F. Domain Analysis of NOV9

gnl|Pfam|pfam00069, pkinase, Protein kinase domain. (SEQ ID NO:100)
Length = 256 residues, 100.0% aligned
Score = 165 bits (418), Expect = 3e-42

NOV9	72	FERISELGAGNGGVVTKVQHRPSGLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIV	131
		+ + + + + + + ++ + + + + +	
00069	1	YELGEKLGSGAFGKVYKKGKHDGTGEIVAIIKILKKRSLSEKKRFLREIQILRRLSHPNIV	60
NOV9	132	GFYGAFYSDGEISICMEHMDGGSGLDQVLKEAK-RIPEEILGKVSIAVLRGLAYLREKHQI	190
		+ + + + + + +++ + +	
00069	61	RLLGVFEEDDHLVLMYMEGGDLFDYLRNGLLLSEKEAKKIALQILRGLEYLHSRG-I	119
NOV9	191	MHRDVKPSNILVNSRGEIKLCDFGVSGQL---IDSMANSFVGTRSYMAP-----	236
		+ + ++ + + ++ + +	
00069	120	VHRDLKPENILLDENGTVKIADFLARKLESSSYEKLTFVGTPEYMAPEVLEGRGYSSK	179
NOV9	237	-----PPKLPNGVFTPDFQEFVNKCLIK	259
		+ + + + +	
00069	180	VDVWSLGVILYELLTGKLPFPIDPLEELFRIKERPRRLPLPPNCSEELKDLIKCLNK	239
NOV9	260	NPAERADLKMLTNHTFI	276
		+ + + +	
00069	240	DPEKRPTAKEILNHPWF	256

The amino acid sequence of NOV9 has high homology to other proteins as shown in Table 9G.

Table 9G. BLASTX results for NOV9

Sequences producing High-scoring Segment Pairs:	Reading High Frame	Smallest Sum Prob			N
		Score	P(N)		
patp:AA41652 Human MEK2 protein sequenc, Homo Sapi	400 aa.. +3	1194	4.8e-160	1	
patp:AAW88434 Dis ass prot kinase DAPK-3, Homo Sapi	400 aa.. +3	1186	3.3e-159	1	

The protein similarity information, expression pattern, and map location for the NOV9 suggest that NOV9 may have important structural and/or physiological functions characteristic of the Mitogen Activated Protein Kinase Kinase 2 protein family. Therefore, the NOV9 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the NOV9 compositions of the present invention will have efficacy for treatment of patients suffering from atherosclerosis, metabolic diseases, pathogen infections and neurological diseases. The NOV9 nucleic acid encoding Mitogen Activated Protein Kinase Kinase 2-like protein, and the Mitogen Activated Protein Kinase Kinase 2-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV10

A disclosed NOV10 nucleic acid of 1506 nucleotides (also referred to sggc_draft_c333e1_20000804_da2) encoding a zinc finger protein 276 C2H2 type-like protein is shown in Table 10A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 385-387 and ending with a TGA codon at nucleotides 1504-1506. A putative untranslated region upstream from the initiation codon is underlined in Table 10A, and the start and stop codons are in bold letters.

Table 10A. NOV10 Nucleotide Sequence (SEQ ID NO:29)

CGCTGAGGTTTGAGATCTCGAGAGGGTCCCGTACGACGAGCACTGTGAACCTCCGCCTGCTTGTCGGGCTC
ATGGCCCACTGATCCTTTGCAGGGTCCGTGCCAGCCCCACAGGGGCAGAGGAGGAGCGTGTCTGGG
TGAGTCCTCCCCCGTGGAGGGTGGGCTGGGTGCCGACAGCCGTGGATCTGACATCTCTGTTGACTCTCT
GCAGTGGATCTGATCACATCCAGCCCCAGTGCCTGCACGGCTTGGTGGGGTGGGTGCATGGACATGCGGC
CAGCTGCGGGGCCCTACCCACCTTCAGAGGACACTGTCTCCGAGTACTGCGGCGTCATCCAGGTCTGTGT
GGGGCTGCGACACAGGGCCACGACTACACCATGGATACAGCTCCAGCTGCAAGGCCTTCTTGCTGGACAGT
GCGCTGGCAGTCAAGTGGCCATGGGACAAAGAGACGGCGCCACGGCTGCCCCAGCACCGAGGGTGAACCC
TGGGGATGCCCCCTCAGACCTCCCAGGGTAGAGGGACAGGGACCCAGTTGGGGCTGAGACCAAGACCCTGC
CCAGCAGCGATGTGGCCAGCCTCCTTCGGACAGCGACGCGTGGGGCCAGGTCGGGCTTCCACCTCAG
CCAAGCCTGCCCCCTTTCAGGGGCCCCAGGGCAGTTGGGTGAGAAGCAGCTTCCATCTTCAACCTCGGATGA
TCGGGTAAAAGACGAGTTCACTGACCTTTCTGAGGGAGACGCTTTGAGTGAAGATGAAAATGACAAGAAGC
AAAATGCCAGTCTTCGGACGAGTCTTTGAGCCTTACCCAGAAAGGAAAGTCTCTGGTAAGAAGAGTGAA
AGCAAAGAAGCCAAGAAGTCTGAAGAACCAAGAATTCCGAAGAAGCCGGGACCAAGCCCGGATGGAAGAA
GAAGCTTCGTTGTGAGAGGGAGGAGCTTCCACCATCTACAAGTGTCTTACCAGGGCTGCACGGCCGTGT
ACCGAGGCGCTGACGGCATGAAGAAGCACATCAAGGAGCACCAGAGGAGGTCCGGAGCGGCCCTGCCCC
CACCTTGGCTGCAACAAGGTTTTCATGATCGACCGCTACCTGCAGCGCCACGTGAAGCTCATCCACACAGA
GGTGGGAACTATATCTGTGACGAATGTGGACAAACCTTCAAGCAGCGGAAGCACCTTCTCGTCCACCAA
TGCGCATTTCCGGAGCCAAGCCTTTGAGTGTGAGGTCTGTGGTTCCAGTGCAGGCAGCGGGCATCCCTC
AAGTACCATGACCAACACAAGGCTGAGACTGAGCTGGACTTTGCCTGTGACCAAGTGTGGCCGGCGGTT
TGAGAAGGCCACAACCTCAATGTACATGTCCATGGTGCACCCGCTGACACAGACCCAGGACAAGGCC

TGCCCCCTGGAGGCGGAACCACTGGGCCACCGAGCCCCTCTGTGACCACAGAGGCCAGGCGGTGAAG
CCCGAACCACCTGA

The disclosed NOV10 nucleic acid sequence, localized to chromosome 16, has 271 of 271 bases (100%) identical *Homo sapiens* Fanconi anaemia group A gene, exons 39, 40, 41, 42 and 43 mRNA (gb:GENBANK-ID:HSZ83095|acc:Z83095) ($E = 9.4e^{-77}$).

5 A disclosed NOV10 polypeptide (SEQ ID NO:30) encoded by SEQ ID NO:29 is 373 amino acid residues and is presented using the one-letter amino acid code in Table 10B. Signal P, Psort and/or Hydropathy results predict that NOV10 does not contain a signal peptide and is likely to be localized at the mitochondrial matrix space with a certainty of 0.5517.

Table 10B. Encoded NOV10 protein sequence (SEQ ID NO:30).

MDTSSSKAFLLDSALAVKWPWDKETAPRLPQHRGWNPGDAPQTSQGRGTGTPVGAETKTLPSSTDVAQPP
SDSDAVGPRSGFPPQPSLPLCRAPQGLGEKQLPSSTSDDRVKDEFSDLSEGDVLSDEDNDKKQNAQSSDE
SFEPYPERKVSQKSESKEAKKSEEPRIKKPGPKPGWKKLRCEEREELPTIYKCPYQGCTAVYRGADGM
KKHIKEHHEEVRERPCPHPGCNKVFMDRYLQRHVKLIHTEVRNYICDECGQTFKQRKHLVHQMHRHSGA
KPLQCEVCGFQCRQRASLKYHMTKHAETELDFACDQCGRRFKAHNLNVHMSMVHPLTQTQDKALPLEA
EPPPGPPSPSVTTEGQAVKPEPT

10 The NOV10 amino acid sequence has 310 of 373 amino acid residues (83%) identical to, and 325 of 373 amino acid residues (87%) similar to, the *Mus musculus* 372 amino acid residue zinc finger protein 276 C2H2 type (ptnr:TREMBLNEW-ACC:AAG01634)($E = 6.3e^{-169}$).

15 NOV10 is expressed in at least the following tissues: bone marrow, brain, cervix, colon, coronary artery, heart, hypothalamus, kidney, lymph node, lung, ovary, peripheral blood, prostate, testis, thyroid, tonsils, uterus and whole organism.

The disclosed NOV10 polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 10C.

Table 10C. BLAST results for NOV10

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi.10048420 ref NP_065243.1 	zinc finger protein (C2H2 type) 276 [Mus musculus]	372	310/374 (82%)	325/374 (86%)	1e-155
gi.11611571 dbj BAB19000.1 (AB052145)	hypothetical protein [Macaca fascicularis]	298	251/253 (99%)	252/253 (99%)	1e-121
gi.14776742 ref XP_047520.1 	hypothetical protein XP_047520 [Homo sapiens]	400	253/253 (100%)	253/253 (100%)	1e-120
gi.11611570 dbj BAB18999.1 (AB052145)	hypothetical protein [Macaca fascicularis]	280	104/110 (94%)	106/110 (95%)	8e-53

gi 15559662 gb AAH14187.1 AAH14187 (BC014187)	Unknown (protein for MGC:20975) [Homo sapiens]	615	86/226 (38%)	127/226 (56%)	7e-38
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The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 10D.

Table 10D. ClustalW Analysis of NOV10

- 1) Novel NOV10 (SEQ ID NO:30)
- 2) gi|10048420|ref|NP_065243.1| zinc finger protein (C2H2 type) 276 [Mus musculus] (SEQ ID NO:80)
- 3) gi|11611571|dbj|BAB19000.1| (AB052145) hypothetical protein [Macaca fascicularis] (SEQ ID NO:81)
- 4) gi|14776742|ref|XP_047520.1| hypothetical protein XP_047520 [Homo sapiens] (SEQ ID NO:82)
- 5) gi|11611570|dbj|BAB18999.1| (AB052145) hypothetical protein [Macaca fascicularis] (SEQ ID NO:83)
- 6) gi|15559662|gb|AAH14187.1|AAH14187 (BC014187) Unknown (protein for MGC:20975) [Homo sapiens] (SEQ ID NO:84)

NOV10	1	-----	1
gi 10048420	1	-----	1
gi 11611571	1	-----	1
gi 14776742	1	-----	1
gi 11611570	1	-----	1
gi 15559662	1	MAERALEPEAEAEAGAGGEEAAEEGAAGRKARGRPRLTESDRARRRLESRKKYDVRV	60
NOV10	1	-----	1
gi 10048420	1	-----	1
gi 11611571	1	-----	1
gi 14776742	1	-----	1
gi 11611570	1	-----	1
gi 15559662	61	YLGEAHGPVWDLRRRSGWSDAKLAAYLISLERGQSRHGKPWEQVPKKPKRKKRRRRNV	120
NOV10	1	-----MDTSS-----SCKAF	10
gi 10048420	1	-----MDTAS-----SCRAL	10
gi 11611571	1	-----	1
gi 14776742	1	-----MDMRPAAGPCPTFRGH	16
gi 11611570	1	-----	1
gi 15559662	121	NCLKNVVIWYEDHKHRCPEPHLAELDPTFGLYTTAVWQCEAGHRYFQDLHSPLKPLSDS	180
NOV10	11	LLDSALAVKWPWD-----KETAPRLPQHRGWNPGDAPQTSQGRGTGTPVG-AETKTLP	62
gi 10048420	11	FLDSALAVKAWG-----KDLSPRLAQNSESNPTGAASRLCQ-ARETQVG-SETKTLP	61
gi 11611571	1	-----	1
gi 14776742	17	CPPSTAASSRSCGAATRATTPWIPAPAARPCSWTVRWQSSGHG-TKRRRHG-CPSTEGG	74
gi 11611570	1	-----MGHCRLCHGKFSSRSLRG-ISERAPG-ASVERP	31
gi 15559662	181	DPDSKVGNGLVAGSSDSSSSGSASDSESPGQPVKAAAAAATPTSPVGSGLITQE	240
NOV10	63	STDVAQPPSDSDAVGPR-----	79
gi 10048420	62	SVDVALLHSHGDSVGPG-----	78
gi 11611571	1	-----	1
gi 14776742	75	TLCMPLRPPRVEGQGPQ-----	91
gi 11611570	32	SAEERVLVRDFQR-L-----	45
gi 15559662	241	GVHIFDFDVHVESLAEQGTPLCSNPAGNGPEALETVVCVPVPVQVAGPSALFENVPOEA	300
NOV10	80	SG-----FPPQPSLPLCRAPG-----QLGEKQLPSSTSD	109
gi 10048420	79	LG-----PC-----TQPHLAPSEAPG-----QLGETQVPSSTSD	108
gi 11611571	1	-----MRPSLLQTATRWGPGRASHLSQACPSAGPQGS	32
gi 14776742	92	LGLRPRPCPARMWPSLLRTATRWGPGRASHLSQACPFAGPQGS	134
gi 11611570	46	LG-----VAVRQDPA-----LSQFVCKS	63
gi 15559662	301	LGEVVASCPMPGMVPGSQVITAGPGYDALTAEGIHLNMAAGSGVPGSGLGEEVPCAMME	360
NOV10	109	-----RVKDEFSDLSEGDVLSSEENDKKQ-----NAOSSDESFEYPYPERKVSGKKS	155
gi 10048420	108	-----RVKDEFSDLSEGDVLSSEENDKKQ-----TPOSSDESFEYPYPERKVSGKKS	154
gi 11611571	32	-----WVRSRSHLQPRMIGDVLSEENDKKQ-----NAOSSDESFEYPYPERKVSGKKS	80
gi 14776742	134	-----WVRSRSHLQPRMIGDVLSEENDKKQ-----NAOSSDESFEYPYPERKVSGKKS	182
gi 11611570	63	-----CHACTYQCHSLLSRSLQRVNVSPGT-----RRKPCAQVGAQLPAGAE	106
gi 15559662	361	GVAAYTQTEPEGSQPSMTDATAVAGIEFKKEKEDLCLKKEKEEPVAPELATTPESAE	420

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NOV10      156  ESKFAKSEEP-----RIRKKPGPKPGWKKKLRCEBELPTIYKCPYQGCTAVYRG 206
gi|10048420| 155  EGRFAKRPEEP-----KIRKKPGPKPGWKKKLRCEBELPTIYKCPYQGCTAVYRG 205
gi|11611571| 81   ESKFAKSEEP-----RIRKKPGPKPGWKKKLRCEBELPTIYKCPYQGCTAVYRG 131
gi|14776742| 183  ESKFAKSEEP-----RIRKKPGPKPGWKKKLRCEBELPTIYKCPYQGCTAVYRG 233
gi|11611570| 107  GACLVDLITSS-----PQCLHGLVGVVHGHAAASCRALPHLQRTLSSEYCGVIQA 155
gi|15559662| 421  PEAEADGDELGDSDMSAIYEIPKEPEKRRRSKRSRVMADGLLEMFHCPYEGCSQVYVA 480

NOV10      207  ADGMKKHIKEHHHEEVRERPCPHPGCNKVFMDRYLQRHVKLIHTEVRNYICDECGQTFKQ 266
gi|10048420| 206  ADGMKKHIKEHHHEEVRERPCPHPGCNKVFMDRYLQRHVKLIHTEVRNYICDECGQTFKQ 265
gi|11611571| 132  ADGMKKHIKEHHHEEVRERPCPHPGCNKVFMDRYLQRHVKLIHTEVRNYICDECGQTFKQ 191
gi|14776742| 234  ADGMKKHIKEHHHEEVRERPCPHPGCNKVFMDRYLQRHVKLIHTEVRNYICDECGQTFKQ 293
gi|11611570| 156  VWG-----CDQGHDTMTDSSSKAFLLDSALAVKW-----PQDKETAPR----- 195
gi|15559662| 481  LSSFQNHVNLVHRKGGTKVCPHPGCCGKKEYLSNHLRRHM-IHSGVREFTCTCGKSFKR 539

NOV10      267  RKHLLVHQMHRHSGAKPLQCEVCGFQCRQRASLKYHMTKHKAETELDFACDQCGRFFEKAH 326
gi|10048420| 266  RNDLLVHQMHRHSGGKPLQCEVCGFQCRQRASLKYHMTKHKAETELDFACDQCGRFFEKAH 325
gi|11611571| 192  RKHLLVHQMHRHSGAKPLQCEVCGFQCRQRASLKYHMTKHKAETELDFACDQCGRFFEKAH 251
gi|14776742| 294  RKHLLVHQMHRHSGAKPLQCEVCGFQCRQRASLKYHMTKHKAETELDFACDQCGRFFEKAH 353
gi|11611570| 195  --LPQHRGWNFGDAPHTSQGKCTGTPVGAETKILPSTDEAOPPSSDAVGPRSGFPQP 252
gi|15559662| 540  KNHLEVHRRTHITGETPLQCEICCYQCRQRASLNWHMKKHTAEVQYNFTCDRCGRFFEKLD 599

NOV10      327  NLNVHMSMVHPELTQTDKALPLEAEPFPGFPPSPSVTTEGQAVKPEPT 373
gi|10048420| 326  NLNVHMSMVHPEWTCQDRALPLEAEPFPGFPPSPSGTMEGQAVKPEPT 372
gi|11611571| 252  NLNVHMSMVHPELTQTDKALPLEAEPFPGFPPSPSVTTEGQAVKPEPT 298
gi|14776742| 354  NLNVHMSMVHPELTQTDKALPLEAEPFPGFPPSPSVTTEGQAVKPEPT 400
gi|11611570| 253  SLPLCGAPGQGEKQVPSSTSDRRRLE----- 280
gi|15559662| 600  SVKFEITLKSHPDHKPT----- 615
```

Table 10E lists the domain description from DOMAIN analysis results against NOV10. This indicates that the NOV10 sequence has properties similar to those of other proteins known to contain these domains.

Table 10E. Domain Analysis of NOV10

gnl|Pfam|pfam00096, zf-C2H2, Zinc finger, C2H2 type. The C2H2 zinc finger is the classical zinc finger domain. The two conserved cysteines and histidines co-ordinate a zinc ion. The following pattern describes the zinc finger. #-X-C-X(1-5)-C-X3-#-X5-#-X2-H-X(3-6)-[H/C] Where X can be any amino acid, and numbers in brackets indicate the number of residues. The positions marked # are those that are important for the stable fold of the zinc finger. The final position can be either his or cys. The C2H2 zinc finger is composed of two short beta strands followed by an alpha helix. The amino terminal part of the helix binds the major groove in DNA binding zinc fingers. (SEQ ID NO:101)
Length = 23 residues, 100.0% aligned
Score = 35.8 bits (81), Expect = 0.004

5

```
NOV10      255  YICDECGQTFKQQRKHLVHQMHRH 277
          || +||++| ++ +| ||
00096      1   YKCPDCGKSFSRKSNLKRHLRTH 23
```

The protein similarity information, expression pattern, and map location for the NOV10 suggest that NOV10 may have important structural and/or physiological functions characteristic of the zinc finger protein 276 C2H2 protein family. Therefore, the NOV10 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For

example, the NOV10 compositions of the present invention will have efficacy for treatment of patients suffering from cancer, trauma, immunological disease, respiratory disease, heart disease, gastro-intestinal diseases, reproductive health, neurological and neurodegenerative diseases, bone marrow transplantation, metabolic and endocrine diseases, allergy and inflammation, nephrological disorders, hematopoietic disorders and urinary system disorders. The NOV10 nucleic acid encoding zinc finger protein 276 C2H2 type-like protein, and the zinc finger protein 276 C2H2 type-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV11

NOV11 includes two novel Thymosin beta-10-like proteins disclosed below. The disclosed proteins have been named NOV11a and NOV11b.

NOV11a

A disclosed NOV11a nucleic acid of 129 nucleotides (also referred to GMAC079400_A) encoding a novel Thymosin beta-10-like protein is shown in Table 11A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 28-30 and ending with a TAA codon at nucleotides 157-159. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 11A, and the start and stop codons are in bold letters.

Table 11A. NOV11a Nucleotide Sequence (SEQ ID NO:31)

ACGGATGGTACCGATTGTTTTAAGAAATGGCAGACAAACAGACGTGGGGGAATCGCCAGCTTCAATA
GGGCCAAGCTGAAGAAAAACGGAGACGCAGGAGAAGAACACCTGCCGACCAAAGAGACCACTGGGCAGAA
CGCGAGTGAAATTCCTAAGAGCCCGGAGGATTCTCTGCCCTCGTC

The disclosed NOV11a nucleic acid sequence has 172 of 190 bases (90%) identical to a *Homo sapiens* Thymosin beta-10 mRNA (GENBANK-ID: S54005) ($E = 3.1e^{-28}$).

A disclosed NOV11a polypeptide (SEQ ID NO:32) encoded by SEQ ID NO:31 is 43 amino acid residues and is presented using the one-letter amino acid code in Table 11B. Signal P, Psort and/or Hydropathy results predict that NOV11a does not contain a signal peptide and is likely to be localized to the nucleus with a certainty of 0.5426

Table 11B. Encoded NOV11a protein sequence (SEQ ID NO:32).

MADKPDVGGIASFNRAKLKKTETQEKNTLPTKETTGQKRSEIS

The NOV11a amino acid sequence has 37 of 44 amino acid residues (84%) identical to, and 40 of 44 amino acid residues (90%) similar to, the *Rattus norvegicus* 44 amino acid

residue Thymosin beta-10 protein (A27266) ($E = 2.4e^{-12}$). The global sequence homology is 88.372% amino acid homology and 86.047% amino acid identity.

NOV11a is predicted to be expressed in the Metastatic Melanoma tissues because of the expression pattern of a closely related *Homo sapiens* Thymosin beta-10 homolog (GENBANK-ID: S54005).

NOV11b

A disclosed NOV11b nucleic acid of 173 nucleotides (also referred to CG109754-01) encoding a novel Thymosin beta-10-like protein is shown in Table 11C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 27-29 and ending with a TAA codon at nucleotides 156-158. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 11C, and the start and stop codons are in bold letters.

Table 11C. NOV11b Nucleotide Sequence (SEQ ID NO:33)

CGGATGGTACCGATTGTTTTAAGAAAATGGCAGACAAACCAGACGTGGGGGAATCGCCAGCTTCAATAGG
GCCAAGCTGAAGAAACGGAGACGCAGGAGAAGAACACCTGCCGACCAAAGAGACCACTGGGCAGAAGCG
GAGTGAAATTCCTAAGAGCCCGAGGATT

The disclosed NOV11b nucleic acid sequence, localized to chromosome 2, has 155 of 168 bases (92%) identical to a *Homo sapiens* Thymosin beta-10 mRNA (gb:GENBANK-ID:HUMTHMBX|acc:M92381.1) ($E = 4.1e^{-25}$).

A disclosed NOV11b polypeptide (SEQ ID NO:34) encoded by SEQ ID NO:33 is 43 amino acid residues and is presented using the one-letter amino acid code in Table 11D. Signal P, Psort and/or Hydropathy results predict that NOV11b does not contain a signal peptide and is likely to be localized to the nucleus with a certainty of 0.5426. Although PSORT suggests the NOV11b polypeptide may be localized in the nucleus, the NOV11b protein is similar to the Thymosin family, some members of which are released extracellularly. Therefore it is likely that this novel Thymosin Beta 10-like protein is localized to the extracellular space.

Table 11D. Encoded NOV11b protein sequence (SEQ ID NO:34).

MADKPDVGGIASFNRAKLKKTETQEKNTLPTKETTGQKRSEIS

The NOV11b amino acid sequence has 36 of 43 amino acid residues (83%) identical to, and 39 of 43 amino acid residues (90%) similar to, the *Homo sapiens* 43 amino acid residue Thymosin beta-10 protein (ptnr:SWISSNEW-ACC:P13472) ($E = 1.7e^{-12}$). NOV11b protein is 43 amino acids long, which is the same length as public protein P13472. NOV11b

protein differs at eight amino acid positions. NOV11b begins with a methionine that the public GenBank submission is lacking. In addition to this, there are six single amino acid changes (M6V, E8G, D14N, K15R, I34T, E35G) and a single amino acid deletion (E37-). This number of changes in such a short peptide indicates that NOV11b protein is derived from a different gene than the public protein.

NOV11b is predicted to be expressed in brain and neuroblastoma tissues because of the expression pattern of a closely related *Homo sapiens* Thymosin beta-10 homolog (GENBANK-ID: gb:GENBANK-ID:HUMTHMBX|acc:M92381.1).

NOV11a and NOV11b are very closely homologous as is shown in the amino acid alignment in Table 11E.

Table 11E Nucleic Acid Alignment of NOV11a and NOV11b

	10	20	30	40	50
NOV11A	ACGGATGGTACCGATTGTTTAAAGAAAATGGCAGACAAACCAGACGTGGG				
NOV11B	-CGGATGGTACCGATTGTTTAAAGAAAATGGCAGACAAACCAGACGTGGG				
	60	70	80	90	100
NOV11A	GGGAATCGCCAGCTTCAATAGGGCCAAGCTGAAGAAAACGGAGACGCAGG				
NOV11B	GGGAATCGCCAGCTTCAATAGGGCCAAGCTGAAGAAAACGGAGACGCAGG				
	110	120	130	140	150
NOV11A	AGAAGAACACCCTGCCGACCAAAGAGACCACTGGGCAGAAGCGGAGTGAA				
NOV11B	AGAAGAACACCCTGCCGACCAAAGAGACCACTGGGCAGAAGCGGAGTGAA				
	160	170	180		
NOV11A	ATTTCCTAAGAGCCCGGAGGATTTCCTGCCCTCGTC				
NOV11B	ATTTCCTAAGAGCCCGGAGGATT-----				

Homologies to any of the above NOV11 proteins will be shared by the other NOV11 proteins insofar as they are homologous to each other as shown above. Any reference to NOV11 is assumed to refer to both of the NOV11 proteins in general, unless otherwise noted.

NOV11a also has homology to the amino acid sequences shown in the BLASTP data listed in Table 11F.

Table 11F. BLAST results for NOV11a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 339697 gb AA367.46.1 (M92383)	thymosin beta-10 [Homo sapiens]	49	37/44 (84%)	40/44 (90%)	4e-04
gi 10863895 ref NP_066926.1	thymosin, beta 10 [Homo sapiens]	42	34/42 (80%)	39/42 (91%)	0.002
gi 223789 prf 0912169A	thymosin beta10, Arg [Oryctolagus cuniculus]	44	37/44 (84%)	40/44 (90%)	0.005

gi 2143995 pir I52084	thymosin beta-4 precursor (fragment) [Rattus norvegicus]	43	36/43 (83%)	39/43 (89%)	0.019
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The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 11G.

Table 11G Information for the ClustalW proteins

- 1) NOV11a (SEQ ID NO:32)
- 2) gi|339697|gb,AAA36746.1. (M92383) thymosin beta-10 [Homo sapiens] (SEQ ID NO:85)
- 3) gi|10863895|ref|NP_066926.1. thymosin, beta 10 [Homo sapiens] (SEQ ID NO:86)
- 4) gi|223789|prf|0912169A thymosin beta10,Arg [Oryctolagus cuniculus] (SEQ ID NO:87)
- 5) gi|2143995|pir|I52084 thymosin beta-4 precursor (fragment) [Rattus norvegicus] (SEQ ID NO:88)

NOV11a	1	-----MADKPDVGGIASFNRAKLKKTETQEKNTLPTKETIGQ-KRSEIS	43
gi 339697	1	-----DCFKMADKPDMDGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSSEIS	49
gi 10863895	1	-----MADKPDMDGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSSEIS	44
gi 223789	1	-----ADKPDMDGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSSEIS	43
gi 2143995	1	LFAQLAQLLPATMSDKPDMAEIEKFDKSKLKKKTETQEKNTLPSKETIEQEKQAGES	56

The amino acid sequence of NOV11 has high homology to other proteins as shown in Table 11H.

Table 11H. BLASTX results for NOV11

		Reading High	Smallest Sum		
Sequences producing High-scoring Segment Pairs:		Frame	Prob	P (N)	N
patp:AAV80267 Thymosin beta 4 peptide isoform Tbeta10, Unknown 43 aa..		+1	169	7.2e-12	1

The protein similarity information, expression pattern, and map location for the NOV11 protein and nucleic acid suggest that NOV11 may have important structural and/or physiological functions characteristic of the Thymosin beta 10 family. Therefore, the NOV11 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the NOV11 compositions of the present invention will have efficacy for treatment of patients suffering from prostate cancer, immunological and autoimmune disorders (ie hyperthyroidism), angiogenesis and wound healing, modulation of apoptosis, neurodegenerative and neuropsychiatric disorders, age-related disorders, pathological disorders involving spleen, thymus, lung, and peritoneal macrophages and/or other pathologies and disorders. The NOV11 nucleic acid encoding Thymosin beta 10-like protein, and the Thymosin beta 10-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOVX Nucleic Acids and Polypeptides

One aspect of the invention pertains to isolated nucleic acid molecules that encode NOVX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify NOVX-encoding nucleic acids (*e.g.*, NOVX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of NOVX nucleic acid molecules. As used herein, the term “nucleic acid molecule” is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An NOVX nucleic acid can encode a mature NOVX polypeptide. As used herein, a “mature” form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product “mature” form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a “mature” form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a “mature” form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term “probes”, as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as

approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated NOVX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 as a hybridization probe, NOVX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to NOVX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term “oligonucleotide” refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue.

Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an NOVX polypeptide). A nucleic acid molecule that is complementary to the nucleotide sequence shown NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 or 33 is one that is sufficiently complementary to the nucleotide sequence shown NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 or 33 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, thereby forming a stable duplex.

As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence.

Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. *See e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A “homologous nucleic acid sequence” or “homologous amino acid sequence,” or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of NOVX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA.

Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an NOVX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human NOVX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17,

19, 21, 23, 25, 27, 29, 31 and 33, as well as a polypeptide possessing NOVX biological activity. Various biological activities of the NOVX proteins are described below.

An NOVX polypeptide is encoded by the open reading frame ("ORF") of an NOVX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, e.g., a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human NOVX genes allows for the generation of probes and primers designed for use in identifying and/or cloning NOVX homologues in other cell types, e.g. from other tissues, as well as NOVX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33; or an anti-sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33; or of a naturally occurring mutant of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33.

Probes based on the human NOVX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an NOVX protein, such as by measuring a level of an NOVX-encoding nucleic acid in a sample of cells from a subject e.g., detecting NOVX mRNA levels or determining whether a genomic NOVX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an NOVX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of NOVX" can be prepared by isolating a portion SEQ ID NOS:1, 3, 5, 7, 9, 11,

13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, that encodes a polypeptide having an NOVX biological activity (the biological activities of the NOVX proteins are described below), expressing the encoded portion of NOVX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of NOVX.

5 NOVX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 due to degeneracy of the genetic code and thus encode the same NOVX proteins as that encoded by the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34.

In addition to the human NOVX nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the NOVX polypeptides may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the NOVX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an NOVX protein, preferably a vertebrate NOVX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the NOVX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the NOVX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the NOVX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding NOVX proteins from other species, and thus that have a nucleotide sequence that differs from the human SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the NOVX cDNAs of the invention can be isolated based on their homology to the human NOVX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding NOVX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM

EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. *See, e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). *See, e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of NOVX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by

mutation into the nucleotide sequences SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, thereby leading to changes in the amino acid sequences of the encoded NOVX proteins, without altering the functional ability of said NOVX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the NOVX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the NOVX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity. Such NOVX proteins differ in amino acid sequence from SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34; more preferably at least about 70% homologous SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34; still more preferably at least about 80% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34; even more preferably at least about 90% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34; and most preferably at least about 95% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34.

An isolated nucleic acid molecule encoding an NOVX protein homologous to the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 by standard techniques, such as site-directed mutagenesis and

PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the NOVX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an NOVX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for NOVX biological activity to identify mutants that retain activity. Following mutagenesis SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved “strong” residues or fully conserved “weak” residues. The “strong” group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the “weak” group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, VLIM, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant NOVX protein can be assayed for (i) the ability to form protein:protein interactions with other NOVX proteins, other cell-surface proteins, or biologically-active portions thereof, (ii) complex formation between a mutant NOVX protein and an NOVX ligand; or (iii) the ability of a mutant NOVX protein to bind to an intracellular target protein or biologically-active portion thereof; (e.g. avidin proteins).

In yet another embodiment, a mutant NOVX protein can be assayed for the ability to regulate a specific biological function (*e.g.*, regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire NOVX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an NOVX protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34, or antisense nucleic acids complementary to an NOVX nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an NOVX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the NOVX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the NOVX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of NOVX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of NOVX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of NOVX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified

nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an NOVX protein to thereby inhibit expression of the protein (*e.g.*, by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (*e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector

constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other. See, e.g., Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (See, e.g., Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or a chimeric RNA-DNA analogue (See, e.g., Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330).

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave NOVX mRNA transcripts to thereby inhibit translation of NOVX mRNA. A ribozyme having specificity for an NOVX-encoding nucleic acid can be designed based upon the nucleotide sequence of an NOVX cDNA disclosed herein (*i.e.*, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an NOVX-encoding mRNA. See, e.g., U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* NOVX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, NOVX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the NOVX nucleic acid (e.g., the NOVX promoter and/or enhancers) to form triple helical structures that prevent transcription of the

NOVX gene in target cells. See, e.g., Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, et al. 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the NOVX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. See, e.g., Hyrup, et al., 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (e.g., DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, et al., 1996. *supra*; Perry-O'Keefe, et al., 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of NOVX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of NOVX can also be used, for example, in the analysis of single base pair mutations in a gene (e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S₁ nucleases (See, Hyrup, et al., 1996. *supra*); or as probes or primers for DNA sequence and hybridization (See, Hyrup, et al., 1996, *supra*; Perry-O'Keefe, et al., 1996. *supra*).

In another embodiment, PNAs of NOVX can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of NOVX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (e.g., RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (see, Hyrup, et al., 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, et al., 1996. *supra* and Finn, et al., 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine

phosphoramidite, can be used between the PNA and the 5' end of DNA. *See, e.g.,* Mag, *et al.*, 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.,* Finn, *et al.*, 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.,* Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.,* Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.,* PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.,* Krol, *et al.*, 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g.,* Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

NOVX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of NOVX polypeptides whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34 while still encoding a protein that maintains its NOVX activities and physiological functions, or a functional fragment thereof.

In general, an NOVX variant that preserves NOVX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated NOVX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided

are polypeptide fragments suitable for use as immunogens to raise anti-NOVX antibodies. In one embodiment, native NOVX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, NOVX proteins are produced by recombinant DNA techniques. Alternative to
5 recombinant expression, an NOVX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the NOVX protein is derived, or substantially free from chemical
10 precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of NOVX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of NOVX proteins having less than about 30% (by dry weight) of non-NOVX proteins (also
15 referred to herein as a "contaminating protein"), more preferably less than about 20% of non-NOVX proteins, still more preferably less than about 10% of non-NOVX proteins, and most preferably less than about 5% of non-NOVX proteins. When the NOVX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%,
20 more preferably less than about 10%, and most preferably less than about 5% of the volume of the NOVX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the
25 language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins having less than about 30% (by dry weight) of chemical precursors or non-NOVX chemicals, more preferably less than about 20% chemical precursors or non-NOVX chemicals, still more preferably less than about 10% chemical precursors or non-NOVX chemicals, and most preferably less than about 5% chemical precursors or
30 non-NOVX chemicals.

Biologically-active portions of NOVX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the NOVX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34) that include fewer amino acids than the full-length

NOVX proteins, and exhibit at least one activity of an NOVX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the NOVX protein. A biologically-active portion of an NOVX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native NOVX protein.

In an embodiment, the NOVX protein has an amino acid sequence shown SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34. In other embodiments, the NOVX protein is substantially homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below.

Accordingly, in another embodiment, the NOVX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34, and retains the functional activity of the NOVX proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. *See*, Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension

penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides NOVX chimeric or fusion proteins. As used herein, an NOVX "chimeric protein" or "fusion protein" comprises an NOVX polypeptide operatively-linked to a non-NOVX polypeptide. An "NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an NOVX protein SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34, whereas a "non-NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the NOVX protein, *e.g.*, a protein that is different from the NOVX protein and that is derived from the same or a different organism. Within an NOVX fusion protein the NOVX polypeptide can correspond to all or a portion of an NOVX protein. In one embodiment, an NOVX fusion protein comprises at least one biologically-active portion of an NOVX protein. In another embodiment, an NOVX fusion protein comprises at least two biologically-active portions of an NOVX protein. In yet another embodiment, an NOVX fusion protein comprises at least three biologically-active portions of an NOVX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the NOVX polypeptide and the non-NOVX polypeptide are fused in-frame with one another. The

non-NOVX polypeptide can be fused to the N-terminus or C-terminus of the NOVX polypeptide.

In one embodiment, the fusion protein is a GST-NOVX fusion protein in which the NOVX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant NOVX polypeptides.

In another embodiment, the fusion protein is an NOVX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of NOVX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an NOVX-immunoglobulin fusion protein in which the NOVX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The NOVX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an NOVX ligand and an NOVX protein on the surface of a cell, to thereby suppress NOVX-mediated signal transduction *in vivo*. The NOVX-immunoglobulin fusion proteins can be used to affect the bioavailability of an NOVX cognate ligand. Inhibition of the NOVX ligand/NOVX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the NOVX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-NOVX antibodies in a subject, to purify NOVX ligands, and in screening assays to identify molecules that inhibit the interaction of NOVX with an NOVX ligand.

An NOVX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.*, Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR

BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An NOVX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the NOVX protein.

5 NOVX Agonists and Antagonists

The invention also pertains to variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists. Variants of the NOVX protein can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the NOVX protein). An agonist of the NOVX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the NOVX protein. An antagonist of the NOVX protein can inhibit one or more of the activities of the naturally occurring form of the NOVX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the NOVX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the NOVX proteins.

Variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists can be identified by screening combinatorial libraries of mutants (*e.g.*, truncation mutants) of the NOVX proteins for NOVX protein agonist or antagonist activity. In one embodiment, a variegated library of NOVX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of NOVX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential NOVX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of NOVX sequences therein. There are a variety of methods which can be used to produce libraries of potential NOVX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential NOVX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.*, Narang, 1983. *Tetrahedron* 39: 3;

Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056;
Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the NOVX protein coding sequences can be used
5 to generate a variegated population of NOVX fragments for screening and subsequent
selection of variants of an NOVX protein. In one embodiment, a library of coding sequence
fragments can be generated by treating a double stranded PCR fragment of an NOVX coding
sequence with a nuclease under conditions wherein nicking occurs only about once per
molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded
10 DNA that can include sense/antisense pairs from different nicked products, removing single
stranded portions from reformed duplexes by treatment with S₁ nuclease, and ligating the
resulting fragment library into an expression vector. By this method, expression libraries can
be derived which encodes N-terminal and internal fragments of various sizes of the NOVX
proteins.

15 Various techniques are known in the art for screening gene products of combinatorial
libraries made by point mutations or truncation, and for screening cDNA libraries for gene
products having a selected property. Such techniques are adaptable for rapid screening of the
gene libraries generated by the combinatorial mutagenesis of NOVX proteins. The most
widely used techniques, which are amenable to high throughput analysis, for screening large
20 gene libraries typically include cloning the gene library into replicable expression vectors,
transforming appropriate cells with the resulting library of vectors, and expressing the
combinatorial genes under conditions in which detection of a desired activity facilitates
isolation of the vector encoding the gene whose product was detected. Recursive ensemble
mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the
25 libraries, can be used in combination with the screening assays to identify NOVX variants.
See, e.g., Arkin and Yourvan, 1992. *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, *et*
al., 1993. *Protein Engineering* 6:327-331.

Anti-NOVX Antibodies

Also included in the invention are antibodies to NOVX proteins, or fragments of
30 NOVX proteins. The term "antibody" as used herein refers to immunoglobulin molecules and
immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that
contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such
antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab},

F_{ab}' and F_{(ab)2} fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated NOVX-related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of NOVX-related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human NOVX-related protein sequence will indicate which regions of a NOVX-related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow and Lane, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson

(The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San

Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., MONOCLONAL ANTIBODY PRODUCTION TECHNIQUES AND APPLICATIONS, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, *Nature* 368, 812-13 (1994)) or by covalently joining to the

immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 **Humanized Antibodies**

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)).

Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL

ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (*Bio/Technology* 10, 779-783 (1992)); Lonberg et al. (*Nature* 368 856-859 (1994)); Morrison (*Nature* 368, 812-13 (1994)); Fishwild et al. (*Nature Biotechnology* 14, 845-51 (1996)); Neuberger (*Nature Biotechnology* 14, 826 (1996)); and Lonberg and Huszar (*Intern. Rev. Immunol.* 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins.

The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be

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further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotype to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as

described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

Immunoconjugates

5 The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have
10 been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcumin, croton, saponaria officinalis inhibitor,
15 gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of
bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate
20 (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-
25 2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such
30 streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an NOVX protein is
5 facilitated by generation of hybridomas that bind to the fragment of an NOVX protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an NOVX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-NOVX antibodies may be used in methods known within the art relating to the
10 localization and/or quantitation of an NOVX protein (*e.g.*, for use in measuring levels of the NOVX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for NOVX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds (hereinafter
15 "Therapeutics").

An anti-NOVX antibody (*e.g.*, monoclonal antibody) can be used to isolate an NOVX polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-NOVX antibody can facilitate the purification of natural NOVX polypeptide from cells and of recombinantly-produced NOVX polypeptide expressed in host cells. Moreover,
20 an anti-NOVX antibody can be used to detect NOVX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the NOVX protein. Anti-NOVX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the
25 antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of
suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of
30 suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol, examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I ,
 ^{131}I , ^{35}S or ^3H .

NOVX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an NOVX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell

and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., NOVX proteins, mutant forms of NOVX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of NOVX proteins in prokaryotic or eukaryotic cells. For example, NOVX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, e.g., Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (see, e.g., Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the NOVX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, NOVX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, e.g., Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and

Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, e.g., the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α -fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to NOVX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.*, Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, NOVX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and

"transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in

5 Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate

10 the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding

15 NOVX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) NOVX protein. Accordingly, the invention further provides

20 methods for producing NOVX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding NOVX protein has been introduced) in a suitable medium such that NOVX protein is produced. In another embodiment, the method further comprises isolating NOVX protein from the medium or the host cell.

25 **Transgenic NOVX Animals**

The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which NOVX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous

30 NOVX sequences have been introduced into their genome or homologous recombinant animals in which endogenous NOVX sequences have been altered. Such animals are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. As used herein, a "transgenic animal" is a

non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous NOVX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing NOVX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human NOVX cDNA sequences SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human NOVX gene, such as a mouse NOVX gene, can be isolated based on hybridization to the human NOVX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the NOVX transgene to direct expression of NOVX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the NOVX transgene in its genome and/or expression of NOVX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding NOVX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an NOVX gene into which a deletion, addition or substitution has been

introduced to thereby alter, *e.g.*, functionally disrupt, the NOVX gene. The NOVX gene can be a human gene (*e.g.*, the cDNA of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33), but more preferably, is a non-human homologue of a human NOVX gene. For example, a mouse homologue of human NOVX gene of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 can be used to construct a homologous recombination vector suitable for altering an endogenous NOVX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous NOVX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous NOVX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous NOVX protein). In the homologous recombination vector, the altered portion of the NOVX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the NOVX gene to allow for homologous recombination to occur between the exogenous NOVX gene carried by the vector and an endogenous NOVX gene in an embryonic stem cell. The additional flanking NOVX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g.*, Thomas, *et al.*, 1987. *Cell* 51: 503 for a description of homologous recombination vectors. The vector is then introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced NOVX gene has homologously-recombined with the endogenous NOVX gene are selected. *See, e.g.*, Li, *et al.*, 1992. *Cell* 69: 915.

The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras. *See, e.g.*, Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

5 A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile
10 diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be
15 adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

 Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous
20 preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating
25 action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of
30 surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by

including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an NOVX protein or anti-NOVX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express NOVX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect NOVX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an NOVX gene, and to modulate NOVX activity, as described further, below. In addition, the NOVX proteins can be used to screen drugs or compounds that modulate the NOVX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of NOVX protein or production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-NOVX antibodies of the invention can be used to detect and isolate NOVX proteins and modulate NOVX activity. In yet a further aspect, the invention can be used in methods to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to NOVX proteins or have a stimulatory or inhibitory effect on, *e.g.*, NOVX protein expression or NOVX protein activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an NOVX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries,

while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. See, e.g., Lam, 1997. *Anticancer Drug Design* 12: 145.

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, e.g., nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (e.g., Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an NOVX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the NOVX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the NOVX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the

assay comprises contacting a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein
 5 determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of NOVX protein, or a biologically-active portion thereof,
 10 on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the NOVX protein to bind to or interact with an NOVX target
 15 molecule. As used herein, a "target molecule" is a molecule with which an NOVX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an NOVX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An NOVX target molecule can be a non-NOVX molecule or an
 20 NOVX protein or polypeptide of the invention. In one embodiment, an NOVX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound NOVX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the
 25 association of downstream signaling molecules with NOVX.

Determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by determining the activity of the
 30 target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an NOVX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*,

luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the NOVX protein or biologically-active portion thereof. Binding of the test compound to the NOVX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX can be accomplished, for example, by determining the ability of the NOVX protein to bind to an NOVX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of NOVX protein can be accomplished by determining the ability of the NOVX protein further modulate an NOVX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the NOVX protein to preferentially bind to or modulate the activity of an NOVX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent

such that the membrane-bound form of NOVX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®],
5 Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either NOVX protein or its target molecule to facilitate separation of
10 complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to NOVX protein, or interaction of NOVX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a
15 fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-NOVX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or NOVX protein, and the mixture is
20 incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of NOVX protein binding or
25 activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the NOVX protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated NOVX protein or target molecules can be prepared from biotin-NHS
30 (N-hydroxy-succinimide) using techniques well-known within the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with NOVX protein or target molecules, but which do not interfere with binding of the NOVX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or NOVX protein trapped in

the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the NOVX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the NOVX protein or target molecule.

In another embodiment, modulators of NOVX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of NOVX mRNA or protein in the cell is determined. The level of expression of NOVX mRNA or protein in the presence of the candidate compound is compared to the level of expression of NOVX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of NOVX mRNA or protein expression based upon this comparison. For example, when expression of NOVX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of NOVX mRNA or protein expression. Alternatively, when expression of NOVX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of NOVX mRNA or protein expression. The level of NOVX mRNA or protein expression in the cells can be determined by methods described herein for detecting NOVX mRNA or protein.

In yet another aspect of the invention, the NOVX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with NOVX ("NOVX-binding proteins" or "NOVX-bp") and modulate NOVX activity. Such NOVX-binding proteins are also likely to be involved in the propagation of signals by the NOVX proteins as, for example, upstream or downstream elements of the NOVX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for NOVX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to

interact, *in vivo*, forming an NOVX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with NOVX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the NOVX sequences, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or fragments or derivatives thereof, can be used to map the location of the NOVX genes, respectively, on a chromosome. The mapping of the NOVX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, NOVX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the NOVX sequences. Computer analysis of the NOVX sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the NOVX sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (*e.g.*, human and mouse cells). As hybrids of human and mouse cells grow and divide, they

gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. *See, e.g., D'Eustachio, et al., 1983. Science 220: 919-924.* Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the NOVX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, *see, Verma, et al., HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES* (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such

data are found, *e.g.*, in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the NOVX gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

The NOVX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the NOVX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The NOVX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single

nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining NOVX protein and/or nucleic acid expression as well as NOVX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant NOVX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. For example, mutations in an NOVX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with NOVX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining NOVX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or

prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of NOVX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting NOVX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes NOVX protein such that the presence of NOVX is detected in the biological sample. An agent for detecting NOVX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to NOVX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length NOVX nucleic acid, such as the nucleic acid of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31 and 33, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to NOVX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting NOVX protein is an antibody capable of binding to NOVX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect NOVX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of NOVX mRNA include Northern hybridizations and *in situ*

hybridizations. *In vitro* techniques for detection of NOVX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of NOVX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of NOVX protein include introducing into a subject a labeled anti-NOVX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting NOVX protein, mRNA, or genomic DNA, such that the presence of NOVX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of NOVX protein, mRNA or genomic DNA in the control sample with the presence of NOVX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of NOVX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting NOVX protein or mRNA in a biological sample; means for determining the amount of NOVX in the sample; and means for comparing the amount of NOVX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect NOVX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant NOVX expression or activity in which a test sample is obtained from a subject and NOVX protein or nucleic acid (*e.g.*, mRNA, genomic

the presence of NOVX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant NOVX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant NOVX expression or activity in which a test sample is obtained and NOVX protein or nucleic acid is detected (*e.g.*, wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant NOVX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an NOVX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an NOVX-protein, or the misexpression of the NOVX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (i) a deletion of one or more nucleotides from an NOVX gene; (ii) an addition of one or more nucleotides to an NOVX gene; (iii) a substitution of one or more nucleotides of an NOVX gene, (iv) a chromosomal rearrangement of an NOVX gene; (v) an alteration in the level of a messenger RNA transcript of an NOVX gene, (vi) aberrant modification of an NOVX gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an NOVX gene, (viii) a non-wild-type level of an NOVX protein, (ix) allelic loss of an NOVX gene, and (x) inappropriate post-translational modification of an NOVX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an NOVX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional

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Mutation 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in NOVX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the NOVX gene and detect mutations by comparing the sequence of the sample NOVX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (*see, e.g.*, Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (*see, e.g.*, PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the NOVX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. *See, e.g.*, Myers, *et al.*, 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type NOVX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁ nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. *See, e.g.*, Cotton, *et al.*, 1988. *Proc. Natl. Acad. Sci. USA* 85:

4397; Saleeba, *et al.*, 1992. *Methods Enzymol.* 217: 286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in NOVX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. See, e.g., Hsu, *et al.*, 1994. *Carcinogenesis* 15: 1657-1662. According to an exemplary embodiment, a probe based on an NOVX sequence, e.g., a wild-type NOVX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, e.g., U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in NOVX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. See, e.g., Orita, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton, 1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79. Single-stranded DNA fragments of sample and control NOVX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen, *et al.*, 1991. *Trends Genet.* 7: 5.

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers, *et al.*, 1985. *Nature* 313: 495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner, 1987. *Biophys. Chem.* 265: 12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g., Saiki, et al., 1986. Nature 324: 163; Saiki, et al., 1989. Proc. Natl. Acad. Sci. USA 86: 6230.* Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g., Gibbs, et al., 1989. Nucl. Acids Res. 17: 2437-2448*) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g., Prossner, 1993. Tibtech. 11: 238*). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. *See, e.g., Gasparini, et al., 1992. Mol. Cell Probes 6: 1.* It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g., Barany, 1991. Proc. Natl. Acad. Sci. USA 88: 189.* In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.,* in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an NOVX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which NOVX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on NOVX activity (e.g., NOVX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such treatment, the pharmacogenomics (i.e., the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (e.g., drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See e.g., Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic

polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an NOVX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase NOVX gene expression, protein levels, or upregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting decreased NOVX gene expression, protein levels, or downregulated NOVX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease NOVX gene expression, protein levels, or downregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting

increased NOVX gene expression, protein levels, or upregulated NOVX activity. In such clinical trials, the expression or activity of NOVX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

5 By way of example, and not of limitation, genes, including NOVX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates NOVX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of
10 NOVX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of NOVX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological
15 response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the
20 screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of an NOVX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the
25 post-administration samples; (v) comparing the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the pre-administration sample with the NOVX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of NOVX to higher levels
30 than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of NOVX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant NOVX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Osteodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (i) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to an aforementioned peptide; (iii) nucleic acids encoding an aforementioned peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous recombination (*see, e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be

utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an
5 aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in*
10 *situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant NOVX expression or activity, by administering to the subject an agent that modulates NOVX expression or at least one NOVX activity. Subjects at
15 risk for a disease that is caused or contributed to by aberrant NOVX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the NOVX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of NOVX
20 aberrancy, for example, an NOVX agonist or NOVX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

Therapeutic Methods

25 Another aspect of the invention pertains to methods of modulating NOVX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of NOVX protein activity associated with the cell. An agent that modulates NOVX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate
30 ligand of an NOVX protein, a peptide, an NOVX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more NOVX protein activity. Examples of such stimulatory agents include active NOVX protein and a nucleic acid molecule encoding NOVX that has been introduced into the cell. In another embodiment, the agent inhibits one or more

NOVX protein activity. Examples of such inhibitory agents include antisense NOVX nucleic acid molecules and anti-NOVX antibodies. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an NOVX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., up-regulates or down-regulates) NOVX expression or activity. In another embodiment, the method involves administering an NOVX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant NOVX expression or activity.

Stimulation of NOVX activity is desirable *in situations* in which NOVX is abnormally downregulated and/or in which increased NOVX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (e.g., cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (e.g., preeclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The NOVX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cancer, neurodegenerative disorders. Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic

disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

As an example, a cDNA encoding the NOVX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof.

By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

Both the novel nucleic acid encoding the NOVX protein, and the NOVX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies, which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

Examples

EXAMPLE 1: Identification of NOVX Nucleic Acids

TblastN using CuraGen Corporation's sequence file for polypeptides or homologs was run against the Genomic Daily Files made available by GenBank or from files downloaded from the individual sequencing centers. Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

The novel NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream

sequence available for the reverse primer. PCR primer sequences were used for obtaining different clones. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The PCR product derived from exon linking was cloned into the pCR2.1 vector from Invitrogen. The resulting bacterial clone has an insert covering the entire open reading frame cloned into the pCR2.1 vector. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

Physical clone: Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

Example 2: Identification of Single Nucleotide Polymorphisms in NOVX nucleic acid sequences

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a

"cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

SeqCalling assemblies produced by the exon linking process were selected and extended using the following criteria. Genomic clones having regions with 98% identity to all or part of the initial or extended sequence were identified by BLASTN searches using the relevant sequence to query human genomic databases. The genomic clones that resulted were selected for further analysis because this identity indicates that these clones contain the genomic locus for these SeqCalling assemblies. These sequences were analyzed for putative coding regions as well as for similarity to the known DNA and protein sequences. Programs used for these analyses include Grail, Genscan, BLAST, HMMER, FASTA, Hybrid and other relevant programs.

Some additional genomic regions may have also been identified because selected SeqCalling assemblies map to those regions. Such SeqCalling sequences may have overlapped with regions defined by homology or exon prediction. They may also be included because the location of the fragment was in the vicinity of genomic regions identified by similarity or exon prediction that had been included in the original predicted sequence. The sequence so identified was manually assembled and then may have been extended using one or more additional sequences taken from CuraGen Corporation's human SeqCalling database. SeqCalling fragments suitable for inclusion were identified by the CuraToolsTM program SeqExtend or by identifying SeqCalling fragments mapping to the appropriate regions of the genomic clones analyzed.

The regions defined by the procedures described above were then manually integrated and corrected for apparent inconsistencies that may have arisen, for example, from miscalled

bases in the original fragments or from discrepancies between predicted exon junctions, EST locations and regions of sequence similarity, to derive the final sequence disclosed herein. When necessary, the process to identify and analyze SeqCalling assemblies and genomic clones was reiterated to derive the full length sequence.

5 **Example 3. Quantitative expression analysis of clones in various cells and tissues**

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on a Perkin-Elmer Biosystems ABI PRISM® 7700 Sequence Detection System. Various collections of
10 samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on metabolic diseases), AI_comprehensive_panel
15 (containing normal tissue and samples from autoinflammatory diseases), Panel CNSD.01 (containing samples from normal and diseased brains) and CNS_neurodegeneration_panel (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a
20 guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

First, the RNA samples were normalized to reference nucleic acids such as
25 constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 ul) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (PE Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions. Probes and primers were designed for each assay according to Perkin Elmer Biosystem's *Primer Express* Software package (version I for Apple Computer's
30 Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60° C, primer optimal T_m = 59° C, maximum primer difference = 2° C, probe does not

have 5' G, probe T_m must be 10° C greater than primer T_m , amplicon size 75 bp to 100 bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200nM.

PCR conditions: Normalized RNA from each tissue and each cell line was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). PCR cocktails including two probes (a probe specific for the target clone and another gene-specific probe multiplexed with the target probe) were set up using 1X TaqMan™ PCR Master Mix for the PE Biosystems 7700, with 5 mM MgCl₂, dNTPs (dA, G, C, U at 1:1:1:2 ratios), 0.25 U/ml AmpliTaq Gold™ (PE Biosystems), and 0.4 U/μl RNase inhibitor, and 0.25 U/μl reverse transcriptase. Reverse transcription was performed at 48° C for 30 minutes followed by amplification/PCR cycles as follows: 95° C 10 min, then 40 cycles of 95° C for 15 seconds, 60° C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on these panels are comprised of samples derived from all major organ systems from single adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine,

colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:

ca. = carcinoma,

* = established from metastasis,

5 met = metastasis,

s cell var = small cell variant,

non-s = non-sm = non-small,

squam = squamous,

pl. eff = pl effusion = pleural effusion,

10 glio = glioma,

astro = astrocytoma, and

neuro = neuroblastoma.

General_screening_panel_v1.4

15 The plates for Panel 1.4 include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in Panel 1.4 are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer.

20 Cell lines used in Panel 1.4 are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on Panel 1.4 are comprised of pools of samples derived from all major organ systems from 2 to 5 different adult individuals or

25 fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

Panels 2D and 2.2

30 The plates for Panels 2D and 2.2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from

human malignancies and in cases where indicated many malignant tissues have “matched margins” obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted “NAT” in the results below. The tumor tissue and the “matched margins” are evaluated by two independent pathologists (the surgical pathologists and again by a pathologists at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated “NAT”, for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

Panel 3D

The plates of Panel 3D are comprised of 94 cDNA samples and two control samples. Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1.3D are of the most common cell lines used in the scientific literature.

Panels 4D, 4R, and 4.1D

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4R) or cDNA (Panels 4D/4.1D) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) were employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for

RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5 ng/ml, TNF alpha at approximately 5-10 ng/ml, IFN gamma at approximately 20-50 ng/ml, IL-4 at approximately 5-10 ng/ml, IL-9 at approximately 5-10 ng/ml, IL-13 at approximately 5-10 ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20 ng/ml PMA and 1-2 μ g/ml ionomycin, IL-12 at 5-10 ng/ml, IFN gamma at 20-50 ng/ml and IL-18 at 5-10 ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5 μ g/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol (5.5×10^{-5} M) (Gibco), and 10 mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum

(FCS) (Hyclone, Logan, UT), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco), 50 ng/ml GMCSF and 5 ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50 ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100 ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 μ g/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. Then CD45RO beads were used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 μ g/ml anti-CD28 (Pharmingen) and 3 μ g/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and

resuspended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10 ng/ml. Cells were harvested for RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10^5 - 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (4 ng/ml). IL-12 (5 ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5 ng/ml) and anti-IFN gamma (1 μ g/ml) were used to direct to Th2 and IL-10 at 5 ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (1 ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1 mM dbcAMP at 5×10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10 ng/ml and ionomycin at 1 μ g/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in

DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at -20 degrees C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300 μ l of RNase-free water and 35 μ l buffer (Promega) 5 μ l DTT, 7 μ l RNAsin and 8 μ l DNase were added. The tube was incubated at 37 degrees C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3 M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80 degrees C.

AI_comprehensive panel_v1.0

The plates for AI_comprehensive panel_v1.0 include two control wells and 89 test samples comprised of cDNA isolated from surgical and postmortem human tissues obtained from the Backus Hospital and Clinomics (Frederick, MD). Total RNA was extracted from tissue samples from the Backus Hospital in the Facility at CuraGen. Total RNA from other tissues was obtained from Clinomics.

Joint tissues including synovial fluid, synovium, bone and cartilage were obtained from patients undergoing total knee or hip replacement surgery at the Backus Hospital. Tissue samples were immediately snap frozen in liquid nitrogen to ensure that isolated RNA was of optimal quality and not degraded. Additional samples of osteoarthritis and rheumatoid arthritis joint tissues were obtained from Clinomics. Normal control tissues were supplied by Clinomics and were obtained during autopsy of trauma victims.

Surgical specimens of psoriatic tissues and adjacent matched tissues were provided as total RNA by Clinomics. Two male and two female patients were selected between the ages of 25 and 47. None of the patients were taking prescription drugs at the time samples were

isolated.

Surgical specimens of diseased colon from patients with ulcerative colitis and Crohn's disease and adjacent matched tissues were obtained from Clinomics. Bowel tissue from three female and three male Crohn's patients between the ages of 41-69 were used. Two patients were not on prescription medication while the others were taking dexamethasone, phenobarbital, or tylenol. Ulcerative colitis tissue was from three male and four female patients. Four of the patients were taking lebid and two were on phenobarbital.

Total RNA from post mortem lung tissue from trauma victims was purchased from Clinomics. Emphysema patients ranged in age from 40-70 and all were smokers, this age range was chosen to focus on patients with cigarette-linked emphysema and to avoid those patients with alpha-1 anti-trypsin deficiencies. Asthma patients ranged in age from 36-75, and excluded smokers to prevent those patients that could also have COPD. COPD patients ranged in age from 35-80 and included both smokers and non-smokers. Most patients were taking corticosteroids, and bronchodilators.

In the labels employed to identify tissues in the AI_comprehensive panel_v1.0 panel, the following abbreviations are used:

Syn = Synovial

Normal = No apparent disease

Rep22 /Rep20 = individual patients

RA = Rheumatoid arthritis

Backus = From Backus Hospital

OA = Osteoarthritis

(SS) (BA) (MF) = Individual patients

Adj = Adjacent tissue

Match control = adjacent tissues

-M = Male

-F = Female

COPD = Chronic obstructive pulmonary disease

Panels 5D and 5I

The plates for Panel 5D and 5I include two control wells and a variety of cDNAs isolated from human tissues and cell lines with an emphasis on metabolic diseases. Metabolic tissues were obtained from patients enrolled in the Gestational Diabetes study. Cells were

obtained during different stages in the differentiation of adipocytes from human mesenchymal stem cells. Human pancreatic islets were also obtained.

In the Gestational Diabetes study subjects are young (18 - 40 years), otherwise healthy women with and without gestational diabetes undergoing routine (elective) Caesarean section.

After delivery of the infant, when the surgical incisions were being repaired/closed, the obstetrician removed a small sample (<1 cc) of the exposed metabolic tissues during the closure of each surgical level. The biopsy material was rinsed in sterile saline, blotted and fast frozen within 5 minutes from the time of removal. The tissue was then flash frozen in liquid nitrogen and stored, individually, in sterile screw-top tubes and kept on dry ice for shipment to or to be picked up by CuraGen. The metabolic tissues of interest include uterine wall (smooth muscle), visceral adipose, skeletal muscle (rectus) and subcutaneous adipose. Patient descriptions are as follows:

Patient 2	Diabetic Hispanic, overweight, not on insulin
Patient 7-9	Nondiabetic Caucasian and obese (BMI>30)
Patient 10	Diabetic Hispanic, overweight, on insulin
Patient 11	Nondiabetic African American and overweight
Patient 12	Diabetic Hispanic on insulin

Adiocyte differentiation was induced in donor progenitor cells obtained from Osirus (a division of Clonetics/BioWhittaker) in triplicate except for Donor 3U which had only two replicates. Scientists at Clonetics isolated, grew and differentiated human mesenchymal stem cells (HuMSCs) for CuraGen based on the published protocol found in Mark F. Pittenger, et al., Multilineage Potential of Adult Human Mesenchymal Stem Cells *Science* Apr 2 1999: 143-147. Clonetics provided Trizol lysates or frozen pellets suitable for mRNA isolation and ds cDNA production. A general description of each donor is as follows:

Donor 2 and 3 U	Mesenchymal Stem cells	Undifferentiated Adipose
Donor 2 and 3 AM	Adipose	AdiposeMidway Differentiated
Donor 2 and 3 AD	Adipose	Adipose Differentiated

Human cell lines were generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: kidney proximal convoluted tubule, uterine smooth muscle cells, small intestine, liver HepG2 cancer cells, heart primary stromal cells, and adrenal cortical adenoma cells. These cells are all

cultured under standard recommended conditions and RNA extracted using the standard procedures. All samples were processed at CuraGen to produce single stranded cDNA.

Panel 5I contains all samples previously described with the addition of pancreatic islets from a 58 year old female patient obtained from the Diabetes Research Institute at the University of Miami School of Medicine. Islet tissue was processed to total RNA at an outside source and delivered to CuraGen for addition to panel 5I.

In the labels employed to identify tissues in the 5D and 5I panels, the following abbreviations are used:

GO Adipose = Greater Omentum Adipose

SK = Skeletal Muscle

UT = Uterus

PL = Placenta

AD = Adipose Differentiated

AM = Adipose Midway Differentiated

U = Undifferentiated Stem Cells

Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains two brains from each of the following diagnoses: Alzheimer's disease, Parkinson's disease, Huntington's disease, Progressive Supranuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus palladus, substantia nigra, Brodman Area 4 (primary motor strip), Brodman Area 7 (parietal cortex), Brodman Area 9 (prefrontal cortex), and Brodman area 17 (occipital cortex). Not all brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus palladus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were

examined for neuropathology and found to be free of any pathology consistent with neurodegeneration.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

- 5 PSP = Progressive supranuclear palsy
- Sub Nigra = Substantia nigra
- Glob Palladus= Globus palladus
- Temp Pole = Temporal pole
- Cing Gyr = Cingulate gyrus
- 10 BA 4 = Brodman Area 4

Panel CNS_Neurodegeneration_V1.0

The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically senile plaque load rated as level 3 on a scale of 0-3; 0 = no evidence of plaques, 3 = severe AD senile plaque load). Within each of these brains, the following regions are represented: hippocampus, temporal cortex (Brodmann Area 21), parietal cortex (Brodmann area 7), and occipital cortex (Brodmann area 17). These regions were chosen to encompass all levels of neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the parietal cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within AD patients. Not all brain regions are represented in all cases.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology upon autopsy

5 Control = Control brains; patient not demented, showing no neuropathology

Control (Path) = Control brains; patient not demented but showing severe AD-like pathology

SupTemporal Ctx = Superior Temporal Cortex

Inf Temporal Ctx = Inferior Temporal Cortex

10 NOV1: Calpain-like

Expression of the NOV1 gene (also referred to as 3352274) was assessed using the primer-probe set Ag2003 described in Table 12. Results from RTQ-PCR runs are shown in Tables 13 and 14.

15 Table 12. Probe Name Ag2003

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CAGCCTAATGCTGAAACCTTCT-3'	59.9	22	1117	102
Probe	TET-5'-ATCCTCAGTTCGGTTTAACGCTGCTG-3'-TAMRA	69.2	26	1145	103
Reverse	5'-ATCCTCGTCATCCTCCTCAT-3'	58.5	20	1178	104

Table 13. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3dx4tm5423 t_ag2003_b2		1.3dx4tm5423 t_ag2003_b2
Liver adenocarcinoma	0.0	Kidney (fetal)	0.0
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.0
Adrenal gland	0.0	Renal ca. RXF 393	0.0
Thyroid	0.7	Renal ca. ACHN	0.0
Salivary gland	0.0	Renal ca. UO-31	0.0
Pituitary gland	0.0	Renal ca. TK-10	9.2
Brain (fetal)	0.0	Liver	100.0
Brain (whole)	2.0	Liver (fetal)	34.5
Brain (amygdala)	0.0	Liver ca. (hepatoblast) HepG2	33.7
Brain (cerebellum)	0.0	Lung	17.5
Brain (hippocampus)	0.0	Lung (fetal)	0.0

Brain (substantia nigra)	3.0	Lung ca. (small cell) LX-1	6.3
Brain (thalamus)	0.0	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.0	Lung ca. (s.cell var.) SHP-77	0.0
Spinal cord	0.0	Lung ca. (large cell) NCI-H460	0.0
CNS ca. (glio/astro) U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
CNS ca. (glio/astro) U-118-MG	0.0	Lung ca. (non-s cell) NCI-H23	0.0
CNS ca. (astro) SW1783	0.0	Lung ca (non-s.cell) HOP-62	0.0
CNS ca.* (neuro; met) SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
CNS ca. (astro) SF-539	0.0	Lung ca. (squamous) SW 900	0.0
CNS ca. (astro) SNB-75	0.0	Lung ca. (squamous) NCI-H596	0.0
CNS ca. (glio) SNB-19	0.0	Mammary gland	0.0
CNS ca. (glio) U251	0.0	Breast ca.* (pl. effusion) MCF-7	7.5
CNS ca. (glio) SF-295	0.0	Breast ca * (pl ef) MDA-MB-231	0.0
Heart (fetal)	0.0	Breast ca.* (pl. effusion) T47D	0.0
Heart	6.3	Breast ca. BT-549	0.0
Fetal Skeletal	0.0	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	4.4	Ovarian ca. OVCAR-3	0.6
Thymus	0.0	Ovarian ca. OVCAR-4	0.0
Spleen	9.7	Ovarian ca. OVCAR-5	0.0
Lymph node	0.0	Ovarian ca. OVCAR-8	0.0
Colorectal	0.0	Ovarian ca. IGROV-1	0.0
Stomach	0.0	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	0.0	Uterus	5.1
Colon ca. SW480	0.0	Placenta	7.1
Colon ca.* (SW480 met)SW620	0.0	Prostate	0.0
Colon ca. HT29	2.9	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	11.8
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
83219 CC Well to Mod Diff (ODO3866)	22.9	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	1.4	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma M14	0.0
Bladder	0.0	Melanoma LOX IMVI	0.0
Trachea	5.5	Melanoma* (met) SK-MEL-5	0.0
Kidney	0.0	Adipose	0.6

Table 14. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4dx4tm5530t_ag2003_b2		4dx4tm5530t_ag2003_b2
93768_Secondary Th1_anti-CD28/anti-CD3	7.1	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	93779_HUVEC (Endothelial)_IFN gamma	0.0

93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	9.1	93781_HUVEC (Endothelial)_IL-11	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.0	93583_Lung Microvascular Endothelial Cells_none	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium_none	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0.0	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	17.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	98.9
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium_none	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	24.9
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	1.7	92668_Coronary Artery SMC_resting	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107_astrocytes_resting	0.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	6.5
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	92666_KU-812 (Basophil)_resting	0.0
93354_CD4_none	0.0	92667_KU-812 (Basophil)_PMA/ionomycin	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	4.0	93579_CCD1106 (Keratinocytes)_none	5.9
		93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	28.9
93103_LAK cells_resting	0.0	93791_Liver Cirrhosis	100.0
93788_LAK cells_IL-2	6.5	93792_Lupus Kidney	30.2
93787_LAK cells_IL-2+IL-12	0.0		
93789_LAK cells_IL-2+IFN gamma	0.0	93577_NCI-H292	0.0
93790_LAK cells_IL-2+ IL-18	0.0	93358_NCI-H292_IL-4	0.0
93104_LAK cells_PMA/ionomycin and IL-18	0.0	93360_NCI-H292_IL-9	1.1
93578_NK Cells_IL-2_resting	0.0	93359_NCI-H292_IL-13	0.0
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93357_NCI-H292_IFN gamma	0.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93777_HPAEC_-	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC_IL-1 beta/TNA alpha	0.0

93112_Mononuclear Cells (PBMCs)_resting	0.0	93254_Normal Human Lung Fibroblast_none	0.0
93113_Mononuclear Cells (PBMCs)_PWM	0.0	93253_Normal Human Lung Fibroblast_TNF α (4 ng/ml) and IL-1 β (1 ng/ml)	0.0
93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	93257_Normal Human Lung Fibroblast_IL-4	0.0
93249_Ramos (B cell)_none	0.0	93256_Normal Human Lung Fibroblast_IL-9	0.0
93250_Ramos (B cell)_ionomycin	0.0	93255_Normal Human Lung Fibroblast_IL-13	0.0
93349_B lymphocytes_PWM	5.6	93258_Normal Human Lung Fibroblast_IFN gamma	0.0
93350_B lymphocytes_CD40L and IL-4	1.0	93106_Dermal Fibroblasts CCD1070_resting	0.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	3.1	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0
93356_Dendritic Cells_none	0.0	93772_dermal fibroblast_IFN gamma	0.0
93355_Dendritic Cells_LPS 100 ng/ml	0.0	93771_dermal fibroblast_IL-4	0.0
93775_Dendritic Cells_anti-CD40	0.0	93260_IBD Colitis 2	0.0
93774_Monocytes_resting	6.3	93261_IBD Crohns	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	735010_Colon_normal	14.7
93581_Macrophages_resting	0.0	735019_Lung_none	0.0
93582_Macrophages_LPS 100 ng/ml	0.0	64028-1_Thymus_none	36.1
93098_HUVEC (Endothelial)_none	0.0	64030-1_Kidney_none	0.0
93099_HUVEC (Endothelial)_starved	0.0		

Panel 1.3D Summary Expression of the NOV1 gene appears to be specific to the liver, with the highest expression in normal liver tissue (CT=32.1), and significant expression detected in fetal liver and a liver cancer cell line as well. Since the expression of the NOV1 gene appears to be associated with the liver, it could potentially be used to differentiate between tissues derived from the liver and other tissues. Furthermore, therapeutic modulation of the NOV1 gene may be beneficial in the treatment of liver related disorders, such as liver cirrhosis.

Panel 4D Summary Expression of the NOV1 gene in this panel is restricted to a few samples, with highest expression detected in liver cirrhosis (CT=33.2). This result is in concordance with the liver specific expression seen in Panel 1.3D. Expression of the gene is also detected at low but significant levels in the thymus and TNF-alpha and IL-1beta treated bronchial epithelium. The protein encoded by the NOV1 gene has homology to calcium-

activated neutral proteases (calpain). Calpains have been identified in the trachea and in the lung, and may be involved in tissue destruction. Therapeutic drugs designed with the protein encoded for by the NOV1 gene may be important for the treatment of asthma, emphysema, and liver cirrhosis (Dear et al., A new subfamily of vertebrate calpains lacking a calmodulin-like domain: implications for calpain regulation and evolution. Genomics. 45:175-84, 1997).

NOV2: Epsin-like

Expression of the NOV2 gene (also referred to as 21421174) was assessed using the primer-probe set Ag3088 described in Table BA Results from RTQ-PCR runs are shown in Tables 15, 16, 17, 18 and 19.

Table 15. Probe Name Ag3088

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CACGTTTACAAGCCATGAC-3'	59	20	256	105
Probe	FAM-5'-ATGGAGTACCTCATCAAGACCGGCTC-3'-TAMRA	68.6	26	280	106
Reverse	5'-ATGTTCTCCTTGCACTGCTG-3'	59	20	319	107

Table 16. Panel 1.3D

Tissue Name	Relative Expression(%) 1.3dx4tm5430 f_ag3088_b1	Tissue Name	Relative Expression(%) 1.3dx4tm5430 f_ag3088_b1
Liver adenocarcinoma	37.2	Kidney (fetal)	11.7
Pancreas	19.0	Renal ca. 786-0	11.6
Pancreatic ca. CAPAN 2	31.2	Renal ca. A498	64.4
Adrenal gland	15.5	Renal ca. RXF 393	44.2
Thyroid	15.5	Renal ca. ACHN	25.7
Salivary gland	11.7	Renal ca. UO-31	36.5
Pituitary gland	10.3	Renal ca. TK-10	9.9
Brain (fetal)	46.5	Liver	12.1
Brain (whole)	70.5	Liver (fetal)	21.9
Brain (amygdala)	64.8	Liver ca. (hepatoblast) HepG2	52.1
Brain (cerebellum)	53.4	Lung	17.2
Brain (hippocampus)	77.3	Lung (fetal)	18.6
Brain (substantia nigra)	29.2	Lung ca. (small cell) LX-1	12.4
Brain (thalamus)	55.5	Lung ca. (small cell) NCI-H69	19.1
Cerebral Cortex	84.6	Lung ca. (s.cell var.) SHP-77	24.9
Spinal cord	19.2	Lung ca. (large cell) NCI-H460	18.1
CNS ca. (glio/astro) U87-MG	43.5	Lung ca. (non-sm. cell) A549	24.0
CNS ca. (glio/astro) U-118-MG	100.0	Lung ca. (non-s.cell) NCI-H23	6.0

CNS ca (astro) SW1783	38.8	Lung ca (non-s.cell) HOP-62	11.6
CNS ca * (neuro; met) SK-N-AS	65.9	Lung ca. (non-s.cl) NCI-H522	6.2
CNS ca (astro) SF-539	21.7	Lung ca. (squam.) SW 900	18.0
CNS ca. (astro) SNB-75	64.9	Lung ca. (squam.) NCI-H596	32.0
CNS ca (glio) SNB-19	40.3	Mammary gland	16.8
CNS ca. (glio) U251	40.6	Breast ca.* (pl. effusion) MCF-7	19.7
CNS ca (glio) SF-295	32.1	Breast ca.* (pl.ef) MDA-MB-231	80.4
Heart (fetal)	36.8	Breast ca.* (pl. effusion) T47D	11.9
Heart	22.0	Breast ca. BT-549	44.8
Fetal Skeletal	14.4	Breast ca. MDA-N	12.6
Skeletal muscle	84.5	Ovary	22.2
Bone marrow	12.1	Ovarian ca. OVCAR-3	19.1
Thymus	6.7	Ovarian ca. OVCAR-4	85.5
Spleen	23.1	Ovarian ca. OVCAR-5	21.0
Lymph node	18.7	Ovarian ca. OVCAR-8	9.6
Colorectal	7.7	Ovarian ca. IGROV-1	5.7
Stomach	58.5	Ovarian ca.* (ascites) SK-OV-3	41.0
Small intestine	44.4	Uterus	19.9
Colon ca. SW480	19.0	Placenta	9.8
Colon ca.* (SW480 met)SW620	13.5	Prostate	16.7
Colon ca. HT29	12.1	Prostate ca.* (bone met)PC-3	87.5
Colon ca. HCT-116	19.1	Testis	23.8
Colon ca. CaCo-2	21.9	Melanoma Hs688(A).T	15.0
83219 CC Well to Mod Diff (ODO3866)	16.3	Melanoma* (met) Hs688(B).T	12.5
Colon ca. HCC-2998	9.6	Melanoma UACC-62	31.6
Gastric ca.* (liver met) NCI-N87	41.3	Melanoma M14	36.6
Bladder	22.4	Melanoma LOX IMVI	24.1
Trachea	21.9	Melanoma* (met) SK-MEL-5	15.5
Kidney	24.0	Adipose	8.5

Table 17. Panel 2.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2.2x4tm6408f_ag3088_b1		2.2x4tm6408f_ag3088_b1
Normal Colon GENPAK 061003	26.7	83793 Kidney NAT (OD04348)	94.6
97759 Colon cancer (OD06064)	14.9	98938 Kidney malignant cancer (OD06204B)	12.2
97760 Colon cancer NAT (OD06064)	14.7	98939 Kidney normal adjacent tissue (OD06204E)	29.1
97778 Colon cancer (OD06159)	16.3	85973 Kidney Cancer (OD04450-01)	43.1
97779 Colon cancer NAT (OD06159)	25.3	85974 Kidney NAT (OD04450-03)	40.6
98861 Colon cancer (OD06297-04)	11.5	Kidney Cancer Clontech 8120613	5.7
98862 Colon cancer NAT	15.8	Kidney NAT Clontech 8120614	52.1

(OD06297-015)			
83237 CC Gr.2 ascend colon (ODO3921)	9.0	Kidney Cancer Clontech 9010320	15.5
83238 CC NAT (ODO3921)	10.8	Kidney NAT Clontech 9010321	22.4
97766 Colon cancer metastasis (OD06104)	5.8	Kidney Cancer Clontech 8120607	83.0
97767 Lung NAT (OD06104)	17.5	Kidney NAT Clontech 8120608	35.5
87472 Colon mets to lung (OD04451-01)	23.2	Normal Uterus GENPAK 061018	13.0
87473 Lung NAT (OD04451-02)	19.2	Uterus Cancer GENPAK 064011	12.3
Normal Prostate Clontech A+ 6546-1 (8090438)	22.4	Normal Thyroid Clontech A+ 6570-1 (7080817)	7.5
84140 Prostate Cancer (OD04410)	7.8	Thyroid Cancer GENPAK 064010	12.9
84141 Prostate NAT (OD04410)	7.5	Thyroid Cancer INVITROGEN A302152	28.0
Normal Ovary Res. Gen.	48.3	Thyroid NAT INVITROGEN A302153	7.1
98863 Ovarian cancer (OD06283-03)	10.4	Normal Breast GENPAK 061019	14.9
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	7.6	84877 Breast Cancer (OD04566)	14.5
Ovarian Cancer GENPAK 064008	11.9	Breast Cancer Res. Gen. 1024	30.7
97773 Ovarian cancer (OD06145)	11.7	85975 Breast Cancer (OD04590-01)	60.4
97775 Ovarian cancer NAT (OD06145)	19.8	85976 Breast Cancer Mets (OD04590-03)	25.3
98853 Ovarian cancer (OD06455-03)	14.2	87070 Breast Cancer Metastasis (OD04655-05)	55.0
98854 Ovarian NAT (OD06455-07) Fallopian tube	1.9	GENPAK Breast Cancer 064006	20.4
Normal Lung GENPAK 061010	13.2	Breast Cancer Clontech 9100266	16.3
92337 Invasive poor diff. lung adeno (ODO4945-01)	22.1	Breast NAT Clontech 9100265	7.2
92338 Lung NAT (ODO4945-03)	13.5	Breast Cancer INVITROGEN A209073	7.7
84136 Lung Malignant Cancer (OD03126)	12.2	Breast NAT INVITROGEN A2090734	17.9
84137 Lung NAT (OD03126)	5.6	97763 Breast cancer (OD06083)	29.5
90372 Lung Cancer (OD05014A)	15.3	97764 Breast cancer node metastasis (OD06083)	30.2
90373 Lung NAT (OD05014B)	19.8	Normal Liver GENPAK 061009	50.3
97761 Lung cancer (OD06081)	21.2	Liver Cancer Research Genetics RNA 1026	27.7
97762 Lung cancer NAT (OD06081)	12.8	Liver Cancer Research Genetics RNA 1025	80.2
85950 Lung Cancer (OD04237-01)	5.5	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	51.3
85970 Lung NAT (OD04237-02)	23.6	Paired Liver Tissue Research Genetics RNA 6004-N	7.0
83255 Ocular Mel Met to Liver (ODO4310)	16.4	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	54.3
83256 Liver NAT (ODO4310)	19.3	Paired Liver Tissue Research Genetics RNA 6005-N	100.0
84139 Melanoma Mets to Lung (OD04321)	21.4	Liver Cancer GENPAK 064003	62.4

84138 Lung NAT (OD04321)	7.0	Normal Bladder GENPAK 061001	19.8
Normal Kidney GENPAK 061008	12.8	Bladder Cancer Research Genetics RNA 1023	10.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	59.3	Bladder Cancer INVITROGEN A302173	24.4
83787 Kidney NAT (OD04338)	18.1	Normal Stomach GENPAK 061017	98.0
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	55.8	Gastric Cancer Clontech 9060397	13.5
83789 Kidney NAT (OD04339)	26.5	NAT Stomach Clontech 9060396	41.4
83790 Kidney Ca, Clear cell type (OD04340)	13.5	Gastric Cancer Clontech 9060395	26.0
83791 Kidney NAT (OD04340)	29.0	NAT Stomach Clontech 9060394	37.4
83792 Kidney Ca, Nuclear grade 3 (OD04348)	12.1	Gastric Cancer GENPAK 064005	30.9

Table 18. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4dx4tm5510f_ag3088_b2		4dx4tm5510f_ag3088_b2
93768_Secondary Th1_anti-CD28/anti-CD3	8.7	93100_HUVEC (Endothelial)_IL-1b	6.4
93769_Secondary Th2_anti-CD28/anti-CD3	7.7	93779_HUVEC (Endothelial)_IFN gamma	17.7
93770_Secondary Tr1_anti-CD28/anti-CD3	9.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	12.1
93573_Secondary Th1_resting day 4-6 in IL-2	5.8	93101_HUVEC (Endothelial)_TNF alpha + IL4	16.3
93572_Secondary Th2_resting day 4-6 in IL-2	4.1	93781_HUVEC (Endothelial)_IL-11	14.0
93571_Secondary Tr1_resting day 4-6 in IL-2	4.3	93583_Lung Microvascular Endothelial Cells_none	18.4
93568_primary Th1_anti-CD28/anti-CD3	4.3	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	12.4
93569_primary Th2_anti-CD28/anti-CD3	8.4	92662_Microvascular Dermal endothelium_none	23.4
93570_primary Tr1_anti-CD28/anti-CD3	11.7	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	13.0
93565_primary Th1_resting dy 4-6 in IL-2	21.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	11.9
93566_primary Th2_resting dy 4-6 in IL-2	10.3	93347_Small Airway Epithelium_none	14.4
93567_primary Tr1_resting dy 4-6 in IL-2	7.3	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	44.3
93351_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	12.7	92668_Coronary Artery SMC_resting	24.4
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	10.3	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	12.3

93251_CD8 Lymphocytes_anti-CD28/anti-CD3	7.2	93107_astrocytes_resting	19.9
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	9.4	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	36.7
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	8.5	92666_KU-812 (Basophil)_resting	15.8
93354_CD4_none	3.1	92667_KU-812 (Basophil)_PMA/ionomycin	27.8
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	8.1	93579_CCD1106 (Keratinocytes)_none	14.8
93103_LAK cells_resting	4.9	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	49.4
93788_LAK cells_IL-2	11.3	93791_Liver Cirrhosis	11.6
93787_LAK cells_IL-2+IL-12	14.4	93792_Lupus Kidney	11.6
93789_LAK cells_IL-2+IFN gamma	12.8	93577_NCI-H292	33.5
93790_LAK cells_IL-2+IL-18	9.0	93358_NCI-H292_IL-4	68.3
93104_LAK cells_PMA/ionomycin and IL-18	3.2	93360_NCI-H292_IL-9	41.9
93578_NK Cells_IL-2_resting	4.7	93359_NCI-H292_IL-13	27.9
93109_Mixed Lymphocyte Reaction_Two Way MLR	7.1	93357_NCI-H292_IFN gamma	21.6
93110_Mixed Lymphocyte Reaction_Two Way MLR	6.0	93777_HPAEC_-	13.8
93111_Mixed Lymphocyte Reaction_Two Way MLR	4.9	93778_HPAEC_IL-1 beta/TNFa, alpha	16.4
93112_Mononuclear Cells (PBMCs)_resting	5.0	93254_Normal Human Lung Fibroblast_none	38.7
93113_Mononuclear Cells (PBMCs)_PWM	5.8	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	46.6
93114_Mononuclear Cells (PBMCs)_PHA-L	4.1	93257_Normal Human Lung Fibroblast_IL-4	34.6
93249_Ramos (B cell)_none	23.0	93256_Normal Human Lung Fibroblast_IL-9	20.3
93250_Ramos (B cell)_ionomycin	16.8	93255_Normal Human Lung Fibroblast_IL-13	19.8
93349_B lymphocytes_PWM	7.4	93258_Normal Human Lung Fibroblast_IFN gamma	32.4
93350_B lymphocytes_CD40L and IL-4	5.4	93106_Dermal Fibroblasts CCD1070_resting	48.1
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	12.2	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	39.6
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	10.6	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	23.7
93356_Dendritic Cells_none	10.0	93772_dermal fibroblast_IFN gamma	11.6
93355_Dendritic Cells_LPS 100 ng/ml	8.8	93771_dermal fibroblast_IL-4	23.5
93775_Dendritic Cells_anti-CD40	11.9	93260_IBD Colitis 2	5.0
93774_Monocytes_resting	13.5	93261_IBD Crohns	12.2
93776_Monocytes_LPS 50 ng/ml	8.5	735010_Colon_normal	100.0

93581_Macrophages_resting	11.6	735019_Lung_none	11.4
93582_Macrophages_LPS 100 ng/ml	7.4	64028-1_Thymus_none	25.3
93098_HUVEC (Endothelial)_none	43.0	64030-1_Kidney_none	8.4
93099_HUVEC (Endothelial)_starved	43.9		

Table 19. Panel CNS_neurodegeneration_v1.0

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm7048f_ ag3088_a2_s1		tm7048f_ ag3088_a2_s1
AD 1 Hippo	19.7	Control (Path) 3 Temporal Ctx	14.0
AD 2 Hippo	35.6	Control (Path) 4 Temporal Ctx	44.4
AD 3 Hippo	17.9	AD 1 Occipital Ctx	27.8
AD 4 Hippo	17.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	100.0	AD 3 Occipital Ctx	15.6
AD 6 Hippo	61.7	AD 4 Occipital Ctx	92.3
Control 2 Hippo	58.0	AD 5 Occipital Ctx	70.8
Control 4 Hippo	15.2	AD 6 Occipital Ctx	25.9
Control (Path) 3 Hippo	13.1	Control 1 Occipital Ctx	8.7
AD 1 Temporal Ctx	29.1	Control 2 Occipital Ctx	77.7
AD 2 Temporal Ctx	47.3	Control 3 Occipital Ctx	29.6
AD 3 Temporal Ctx	14.7	Control 4 Occipital Ctx	9.8
AD 4 Temporal Ctx	34.1	Control (Path) 1 Occipital Ctx	69.0
AD 5 Inf Temporal Ctx	84.2	Control (Path) 2 Occipital Ctx	16.7
AD 5 Sup Temporal Ctx	47.4	Control (Path) 3 Occipital Ctx	7.0
AD 6 Inf Temporal Ctx	65.5	Control (Path) 4 Occipital Ctx	24.5
AD 6 Sup Temporal Ctx	60.2	Control 1 Parietal Ctx	13.8
Control 1 Temporal Ctx	10.0	Control 2 Parietal Ctx	66.5
Control 2 Temporal Ctx	69.1	Control 3 Parietal Ctx	19.8
Control 3 Temporal Ctx	33.8	Control (Path) 1 Parietal Ctx	63.4
Control 3 Temporal Ctx	17.8	Control (Path) 2 Parietal Ctx	33.1
Control (Path) 1 Temporal Ctx	67.6	Control (Path) 3 Parietal Ctx	8.6
Control (Path) 2 Temporal Ctx	52.5	Control (Path) 4 Parietal Ctx	59.2

Panel 1.3D Summary The NOV2 gene is widely expressed in many of the samples in this panel, with highest expression in a brain cancer cell line (CT = 26). The NOV2 gene is also highly expressed in all the normal tissues originating in the central nervous system, including the amygdala, cerebellum, hippocampus, substantia nigra, thalamus, cerebral cortex and spinal cord. The protein encoded by the NOV2 gene is a homolog of epsin, which is involved in the phagocytosis of macromolecules, and interacts with Huntingtin-interacting protein. Therefore, this gene may play a critical role in the endocytosis of Huntingtin protein

and the etiology of Huntington's disease. Downregulation of this gene or its protein product may be of therapeutic benefit in the treatment of Huntington's disease.

The NOV2 gene is also expressed in many tissues with metabolic function, including adipose, the pancreas, the adrenal, thyroid, and pituitary glands, and skeletal muscle, heart and liver from both fetal and adult sources. Thus, this gene product may be important in the pathogenesis and/or treatment of disease in any or all of these tissues, including obesity and diabetes.

The NOV2 gene is highly expressed in renal, breast, brain, ovarian, lung, colon, kidney, pancreatic and prostate cancer cell lines, when compared to normal kidney, breast, ovary, and prostate tissues, and thus may play a role in cancer of these tissues. The gene may also play a role in metastasis of melanoma as one cell line expresses this gene at a higher level compared to other melanoma cell lines. Based on this expression profile, the expression of the NOV2 gene could be of use as a marker for different grades/ types of these cancers.

Furthermore, since this gene is expressed in multiple fetal tissues and cancer cell lines,

Panel 2.2 Summary Highest expression of the NOV2 gene is detected in liver tissue adjacent to a liver tumor (CT = 27.3). In addition, the level of expression in some lung, breast, liver and kidney cancer tissue samples appears to be increased when compared to the matched normal tissue. The reverse appears to be true for colon, ovary and stomach tissue, where expression is slightly higher in normal tissue than the matched cancer tissues. Thus, based upon its profile, the expression of the NOV2 gene could be of use as a marker for distinguishing some cancers from the normal adjacent tissue or as a marker for different grades/ types of cancer.

Panel 4D Summary The NOV2 gene is most highly expressed in colon (CT=22). Significant expression is also detected in a variety of tissues including fibroblasts, endothelial and epithelial cells, keratinocytes, leukocytes and smooth muscle cells. The protein encoded by the NOV2 gene is a homolog of an EH-domain binding like protein, epsin, thought to be involved in endocytosis. Members of the epsin family have been shown to play an important role in wound healing. Since the NOV2 gene is expressed in several cell types, therapeutics designed with the protein encoded for by this gene may serve important roles in regulating the cellular uptake of bio-therapeutic molecules in general, and specifically in enhancing wound healing.

Panel CNS_neurodegeneration_v1.0 Summary Highest expression of the NOV2 gene is detected in the hippocampus of a patient with Alzheimer's disease (CT=25.6).

However, there is also widespread expression in all the samples in this panel and no specific

association between the expression of this gene and the presence of Alzheimer's disease is observed from these results. These results do however confirm expression of the NOV2 gene in the brains of an additional set of individuals. Please see Panel 1.3D for a discussion of potential utility of this gene in the central nervous system (Rosenthal et al., The epsins define a family of proteins that interact with components of the clathrin coat and contain a new protein module. *J Biol Chem.* 274:33959-65, 1999; Mishra et al., Clathrin- and AP-2-binding sites in HIP1 uncover a general assembly role for endocytic accessory proteins. *J Biol Chem*, 2001; Spradling et al., Epsin 3 is a novel extracellular matrix-induced transcript specific to wounded epithelia. *J Biol Chem.* 276:29257-67, 2001).

10 NOV3: Low Density Lipoprotein B-like

Expression of the NOV3 gene (also referred to as AC025263_da1) was assessed using the primer-probe sets Ag2002 and Ag2452 described in Tables 20 and 21. Results from RTQ-PCR runs are shown in Tables 22, 23, 24 and 25.

15 Table 20. Probe Name Ag2002

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-GCCAGAAAGGCAACTATTCAG-3'	59	21	727	108
Probe	FAM-5'-AACTTCTCAACCAGCCACCATGGT-3'-TAMRA	69.7	26	749	109
Reverse	5'-AGCAACTCCACTAATGAGCAAA-3'	59	22	794	110

Table 21. Probe Name Ag2452

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-AGCAGTGCAGTTGTGAAAGTTT-3'	59.1	22	2053	111
Probe	TET-5'-TGATTCATGGATTCACCCAGTCATTA-3'-TAMRA	65.5	26	2075	112
Reverse	5'-CAGAACTGAGCCAGCATCAT-3'	59	20	2108	113

Table 22. Panel 1.3D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	1.3Dtm3824t_ag2452	1.3Dtm2811f_ag2002
Liver adenocarcinoma	6.1	15.9
Pancreas	3.1	5.0
Pancreatic ca. CAPAN 2	1.7	3.8
Adrenal gland	7.7	12.7
Thyroid	6.7	13.6
Salivary gland	4.9	7.3
Pituitary gland	24.8	23.8

Brain (fetal)	8.9	8.5
Brain (whole)	18.9	33.9
Brain (amygdala)	28.9	19.6
Brain (cerebellum)	9.1	8.5
Brain (hippocampus)	100.0	48.6
Brain (substantia nigra)	4.3	5.3
Brain (thalamus)	13.1	15.4
Cerebral Cortex	41.2	100.0
Spinal cord	5.3	8.5
CNS ca. (glio/astro) U87-MG	5.3	14.4
CNS ca. (glio/astro) U-118-MG	20.0	39.5
CNS ca. (astro) SW1783	10.3	25.5
CNS ca.* (neuro; met) SK-N-AS	34.6	36.9
CNS ca. (astro) SF-539	3.8	12.0
CNS ca. (astro) SNB-75	6.7	33.7
CNS ca. (glio) SNB-19	3.9	16.0
CNS ca. (glio) U251	3.9	0.0
CNS ca. (glio) SF-295	8.2	28.9
Heart (fetal)	9.6	55.1
Heart	2.7	7.2
Fetal Skeletal	24.8	84.1
Skeletal muscle	3.8	8.4
Bone marrow	4.5	3.1
Thymus	3.3	7.5
Spleen	9.0	12.7
Lymph node	4.1	12.9
Colorectal	5.9	18.7
Stomach	5.2	17.7
Small intestine	10.4	10.4
Colon ca. SW480	7.8	34.2
Colon ca.* (SW480 met)SW620	6.0	17.1
Colon ca. HT29	3.8	10.2
Colon ca. HCT-116	5.8	9.2
Colon ca. CaCo-2	5.4	22.2
83219 CC Well to Mod Diff (ODO3866)	5.3	15.7
Colon ca. HCC-2998	10.7	14.9
Gastric ca * (liver met) NCI-N87	10.7	31.6
Bladder	3.8	5.3
Trachea	13.2	14.0
Kidney	2.3	3.3
Kidney (fetal)	5.9	9.7
Renal ca. 786-0	2.7	6.8
Renal ca. A498	14.8	34.9
Renal ca. RXF 393	1.3	6.9

Renal ca. ACHN	1.4	24.5
Renal ca. UO-31	3.7	15.5
Renal ca. TK-10	4.6	14.9
Liver	2.9	2.8
Liver (fetal)	7.1	7.9
Liver ca. (hepatoblast) HepG2	5.8	28.1
Lung	11.7	7.5
Lung (fetal)	7.6	14.6
Lung ca. (small cell) LX-1	3.1	16.6
Lung ca. (small cell) NCI-H69	14.7	36.1
Lung ca. (s.cell var.) SHP-77	15.6	30.6
Lung ca. (large cell) NCI-H460	2.2	4.5
Lung ca. (non-sm. cell) A549	8.2	12.0
Lung ca. (non-s.cell) NCI-H23	3.8	15.4
Lung ca. (non-s.cell) HOP-62	5.1	21.8
Lung ca. (non-s cl) NCI-H522	5.5	18.3
Lung ca. (squamous) SW 900	4.0	9.8
Lung ca. (squamous) NCI-H596	3.1	14.7
Mammary gland	11.2	27.5
Breast ca. * (pl. effusion) MCF-7	7.3	23.7
Breast ca. * (pl.ef) MDA-MB-231	23.7	39.8
Breast ca. * (pl. effusion) T47D	8.4	37.1
Breast ca. BT-549	11.0	16.4
Breast ca. MDA-N	8.7	20.6
Ovary	17.6	52.5
Ovarian ca. OVCAR-3	4.9	19.9
Ovarian ca. OVCAR-4	0.9	3.3
Ovarian ca. OVCAR-5	7.0	32.5
Ovarian ca. OVCAR-8	5.4	14.4
Ovarian ca. IGROV-1	1.9	3.8
Ovarian ca. * (ascites) SK-OV-3	4.4	12.0
Uterus	7.6	14.2
Placenta	7.9	13.2
Prostate	6.0	6.8
Prostate ca. * (bone met) PC-3	8.1	18.4
Testis	10.6	19.6
Melanoma Hs688(A).T	3.7	28.9
Melanoma* (met) Hs688(B).T	2.3	45.7
Melanoma UACC-62	1.1	3.3
Melanoma M14	1.2	3.5
Melanoma LOX IMVI	9.1	6.7
Melanoma* (met) SK-MEL-5	12.9	13.7
Adipose	2.6	4.6

Table 23. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2Dtm3825t_ag2452		2Dtm3825t_ag2452
Normal Colon GENPAK 061003	100.0	Kidney NAT Clontech 8120608	24.5
83219 CC Well to Mod Diff (ODO3866)	18.2	Kidney Cancer Clontech 8120613	51.1
83220 CC NAT (ODO3866)	19.1	Kidney NAT Clontech 8120614	29.1
83221 CC Gr.2 rectosigmoid (ODO3868)	8.0	Kidney Cancer Clontech 9010320	19.3
83222 CC NAT (ODO3868)	6.0	Kidney NAT Clontech 9010321	31.4
83235 CC Mod Diff (ODO3920)	23.3	Normal Uterus GENPAK 061018	6.8
83236 CC NAT (ODO3920)	24.0	Uterus Cancer GENPAK 064011	32.1
83237 CC Gr.2 ascend colon (ODO3921)	91.4	Normal Thyroid Clontech A+ 6570-1	29.9
83238 CC NAT (ODO3921)	19.8	Thyroid Cancer GENPAK 064010	28.3
83241 CC from Partial Hepatectomy (ODO4309)	66.4	Thyroid Cancer INVITROGEN A302152	17.1
83242 Liver NAT (ODO4309)	21.2	Thyroid NAT INVITROGEN A302153	29.9
87472 Colon mets to lung (OD04451-01)	24.3	Normal Breast GENPAK 061019	25.7
87473 Lung NAT (OD04451-02)	14.7	84877 Breast Cancer (OD04566)	15.3
Normal Prostate Clontech A+ 6546-1	33.9	85975 Breast Cancer (OD04590-01)	76.8
84140 Prostate Cancer (OD04410)	38.7	85976 Breast Cancer Mets (OD04590-03)	68.3
84141 Prostate NAT (OD04410)	35.8	87070 Breast Cancer Metastasis (OD04655-05)	77.9
87073 Prostate Cancer (OD04720-01)	52.5	GENPAK Breast Cancer 064006	14.2
87074 Prostate NAT (OD04720-02)	68.3	Breast Cancer Res. Gen. 1024	24.3
Normal Lung GENPAK 061010	35.8	Breast Cancer Clontech 9100266	68.3
83239 Lung Met to Muscle (ODO4286)	28.3	Breast NAT Clontech 9100265	31.6
83240 Muscle NAT (ODO4286)	17.8	Breast Cancer INVITROGEN A209073	35.4
84136 Lung Malignant Cancer (OD03126)	35.6	Breast NAT INVITROGEN A2090734	22.8
84137 Lung NAT (OD03126)	45.1	Normal Liver GENPAK 061009	9.6
84871 Lung Cancer (OD04404)	17.9	Liver Cancer GENPAK 064003	9.3
84872 Lung NAT (OD04404)	18.0	Liver Cancer Research Genetics RNA 1025	9.7
84875 Lung Cancer (OD04565)	6.9	Liver Cancer Research Genetics RNA 1026	9.6
84876 Lung NAT (OD04565)	8.2	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	13.6
85950 Lung Cancer (OD04237-01)	50.0	Paired Liver Tissue Research Genetics RNA 6004-N	18.8
85970 Lung NAT (OD04237-02)	16.8	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	10.3

83255 Ocular Mel Met to Liver (ODO4310)	19.9	Paired Liver Tissue Research Genetics RNA 6005-N	1.7
83256 Liver NAT (ODO4310)	18.6	Normal Bladder GENPAK 061001	53.2
84139 Melanoma Mets to Lung (OD04321)	35.1	Bladder Cancer Research Genetics RNA 1023	37 1
84138 Lung NAT (OD04321)	35.1	Bladder Cancer INVITROGEN A302173	26 6
Normal Kidney GENPAK 061008	57.4	87071 Bladder Cancer (OD04718-01)	46.3
83786 Kidney Ca, Nuclear grade 2 (OD04338)	58.2	87072 Bladder Normal Adjacent (OD04718-03)	24.8
83787 Kidney NAT (OD04338)	30.1	Normal Ovary Res. Gen.	41.8
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	26.4	Ovarian Cancer GENPAK 064008	54.0
83789 Kidney NAT (OD04339)	35 4	87492 Ovary Cancer (OD04768-07)	76.8
83790 Kidney Ca, Clear cell type (OD04340)	38.7	87493 Ovary NAT (OD04768-08)	10.5
83791 Kidney NAT (OD04340)	28 7	Normal Stomach GENPAK 061017	33.0
83792 Kidney Ca, Nuclear grade 3 (OD04348)	18 3	Gastric Cancer Clontech 9060358	11 5
83793 Kidney NAT (OD04348)	25.7	NAT Stomach Clontech 9060359	28.5
87474 Kidney Cancer (OD04622-01)	18.4	Gastric Cancer Clontech 9060395	35.1
87475 Kidney NAT (OD04622-03)	7.0	NAT Stomach Clontech 9060394	40 3
85973 Kidney Cancer (OD04450-01)	25.7	Gastric Cancer Clontech 9060397	71.7
85974 Kidney NAT (OD04450-03)	24.1	NAT Stomach Clontech 9060396	18.2
Kidney Cancer Clontech 8120607	13 2	Gastric Cancer GENPAK 064005	35 1

Table 24. Panel 4D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	4dx4tm5532f_a g2002_a2	4Dtm3826t_ ag2452
93768_Secondary Th1_anti-CD28/anti-CD3	25.4	27.4
93769_Secondary Th2_anti-CD28/anti-CD3	35.8	16.7
93770_Secondary Tr1_anti-CD28/anti-CD3	36.9	46 3
93573_Secondary Th1_resting day 4-6 in IL-2	25.8	13 4
93572_Secondary Th2_resting day 4-6 in IL-2	18.9	17 8
93571_Secondary Tr1_resting day 4-6 in IL-2	23.0	17.0
93568_primary Th1_anti-CD28/anti-CD3	15.9	31 0
93569_primary Th2_anti-CD28/anti-CD3	30.9	26.8
93570_primary Tr1_anti-CD28/anti-CD3	30.2	35 8
93565_primary Th1_resting dy 4-6 in IL-2	77.0	83.5
93566_primary Th2_resting dy 4-6 in IL-2	33.8	39 2
93567_primary Tr1_resting dy 4-6 in IL-2	29.2	23 2
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	26.1	30 1
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	37.1	34 9

93251_CD8 Lymphocytes_anti-CD28/anti-CD3	21.8	16.8
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	26.8	24.3
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	23.1	28.9
93354_CD4_none	22.9	19.6
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	29.2	22.5
93103_LAK cells_resting	16.9	21.5
93788_LAK cells_IL-2	33.2	22.8
93787_LAK cells_IL-2+IL-12	33.1	18.4
93789_LAK cells_IL-2+IFN gamma	35.0	37.9
93790_LAK cells_IL-2+ IL-18	30.1	35.6
93104_LAK cells_PMA/ionomycin and IL-18	5.6	6.0
93578_NK Cells IL-2_resting	24.2	19.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	29.3	28.9
93110_Mixed Lymphocyte Reaction_Two Way MLR	22.3	15.3
93111_Mixed Lymphocyte Reaction_Two Way MLR	21.6	12.1
93112_Mononuclear Cells (PBMCs)_resting	14.6	12.4
93113_Mononuclear Cells (PBMCs)_PWM	22.3	57.8
93114_Mononuclear Cells (PBMCs)_PHA-L	11.5	28.7
93249_Ramos (B cell)_none	27.1	21.5
93250_Ramos (B cell)_ionomycin	16.9	66.9
93349_B lymphocytes_PWM	23.6	65.5
93350_B lymphocytes_CD40L and IL-4	23.6	27.5
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	8.8	6.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMA/ionomycin	8.3	6.6
93356_Dendritic Cells_none	14.0	10.1
93355_Dendritic Cells_LPS 100 ng/ml	14.0	10.4
93775_Dendritic Cells_anti-CD40	19.4	15.0
93774_Monocytes_resting	25.3	22.5
93776_Monocytes_LPS 50 ng/ml	25.4	20.0
93581_Macrophages_resting	21.6	24.8
93582_Macrophages_LPS 100 ng/ml	16.5	13.7
93098_HUVEC (Endothelial)_none	31.1	36.9
93099_HUVEC (Endothelial)_starved	45.2	55.9
93100_HUVEC (Endothelial)_IL-1b	15.8	24.7
93779_HUVEC (Endothelial)_IFN gamma	37.6	45.4
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	29.3	27.4
93101_HUVEC (Endothelial)_TNF alpha + IL4	27.6	20.4
93781_HUVEC (Endothelial)_IL-11	13.9	11.7
93583_Lung Microvascular Endothelial Cells_none	21.2	26.4
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	29.0	34.9
92662_Microvascular Dermal endothelium_none	25.5	36.3
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	25.7	28.7
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	22.9	6.2

93347_Small Airway Epithelium_none	18.8	17.7
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	44.4	51.1
92668_Coronary Artery SMC_resting	28.0	45.4
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	22.3	25.0
93107_astrocytes_resting	41.0	24.0
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	58.4	17.4
92666_KU-812 (Basophil)_resting	28.6	31.0
92667_KU-812 (Basophil)_PMA/ionomycin	63.5	65.1
93579_CCD1106 (Keratinocytes)_none	17.0	18.9
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	79.9	2.6
93791_Liver Cirrhosis	16.7	3.3
93792_Lupus Kidney	21.9	5.1
93577_NCI-H292	24.0	46.3
93358_NCI-H292_IL-4	24.3	42.6
93360_NCI-H292_IL-9	25.2	58.6
93359_NCI-H292_IL-13	11.7	32.3
93357_NCI-H292_IFN gamma	14.7	37.9
93777_HPAEC_-	23.1	25.7
93778_HPAEC_IL-1 beta/TNF alpha	39.3	44.4
93254_Normal Human Lung Fibroblast_none	40.6	26.2
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	71.3	31.6
93257_Normal Human Lung Fibroblast_IL-4	52.7	66.4
93256_Normal Human Lung Fibroblast_IL-9	29.9	67.8
93255_Normal Human Lung Fibroblast_IL-13	33.0	35.1
93258_Normal Human Lung Fibroblast_IFN gamma	45.0	77.4
93106_Dermal Fibroblasts CCD1070_resting	56.3	83.5
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	84.6	100.0
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	39.7	45.4
93772_dermal fibroblast_IFN gamma	15.5	19.5
93771_dermal fibroblast_IL-4	29.2	42.3
93260_IBD Colitis 2	4.7	2.2
93261_IBD Crohns	7.2	4.7
735010_Colon_normal	100.0	37.9
735019_Lung_none	15.0	26.6
64028-1_Thymus_none	39.9	55.1
64030-1_Kidney_none	35.3	67.8

Table 25. Panel CNS_neurodegeneration_v1.0

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm6902t_ag2452_a2s2		tm6902t_ag2452_a2s2
AD 1 Hippo	8.0	Control (Path) 3 Temporal Ctx	4.2
AD 2 Hippo	36.4	Control (Path) 4 Temporal Ctx	35.8

AD 3 Hippo	2.9	AD 1 Occipital Ctx	5.2
AD 4 Hippo	8.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	52.3	AD 3 Occipital Ctx	2.1
AD 6 Hippo	47.1	AD 4 Occipital Ctx	28.1
Control 2 Hippo	37.4	AD 5 Occipital Ctx	15.8
Control 4 Hippo	7.7	AD 6 Occipital Ctx	49.3
Control (Path) 3 Hippo	3.6	Control 1 Occipital Ctx	2.2
AD 1 Temporal Ctx	7.9	Control 2 Occipital Ctx	65.3
AD 2 Temporal Ctx	49.1	Control 3 Occipital Ctx	10.0
AD 3 Temporal Ctx	4.1	Control 4 Occipital Ctx	5.3
AD 4 Temporal Ctx	28.4	Control (Path) 1 Occipital Ctx	87.2
AD 5 Inf Temporal Ctx	76.5	Control (Path) 2 Occipital Ctx	9.0
AD 5 Sup Temporal Ctx	32.8	Control (Path) 3 Occipital Ctx	1.5
AD 6 Inf Temporal Ctx	46.7	Control (Path) 4 Occipital Ctx	12.0
AD 6 Sup Temporal Ctx	42.1	Control 1 Parietal Ctx	5.0
Control 1 Temporal Ctx	3.7	Control 2 Parietal Ctx	28.9
Control 2 Temporal Ctx	51.3	Control 3 Parietal Ctx	15.5
Control 3 Temporal Ctx	14.0	Control (Path) 1 Parietal Ctx	87.4
Control 4 Temporal Ctx	7.6	Control (Path) 2 Parietal Ctx	24.7
Control (Path) 1 Temporal Ctx	100.0	Control (Path) 3 Parietal Ctx	1.3
Control (Path) 2 Temporal Ctx	45.4	Control (Path) 4 Parietal Ctx	41.9

Panel 1.3D Summary Ag2002/Ag2452 Two experiments with two different probe/primer sets produce results that are in very good agreement, with highest expression in both runs occurring in regions of the brain. Expression of the NOV3 gene is highest in the cerebral cortex (CTs=26) in one run and the hippocampus in the other (CT=27) with significant expression also detected in the amygdala. This expression pattern indicates a functional role for the NOV3 gene product in Alzheimer's disease (AD), since the gene, a low density lipoprotein homolog, is expressed in the regions of the brain important to AD pathology. Increased expression of apolipoprotein B in the serum of Alzheimer's disease, and evidence that LRP contributes to the pathogenesis of Alzheimer's disease suggest a pathological role for the protein encoded by the NOV3 gene. Therefore, the AC024263_A gene product may be a promising antibody or small molecule target for the treatment of Alzheimer's disease.

High levels of expression are also detected in cell lines derived from brain cancer, breast cancer, lung cancer, kidney cancer and melanoma. In addition, the expression in normal ovary seems to be higher than in cell lines derived from ovarian cancer tissues. Thus, the expression of this gene could be of use as a marker or as a therapeutic for these cancers.

The NOV3 gene is widely expressed in tissues with metabolic function and significantly, is expressed at higher levels in fetal skeletal muscle (CTs=27-30) than in adult skeletal muscle (CTs=30-33). This difference in expression suggests that the NOV3 protein product could be involved in muscular growth or development in the fetus and therefore could act in a regenerative capacity in an adult. Thus, therapeutic modulation of the NOV3 gene could be useful in the treatment of muscle related diseases and treatment with the protein product could restore muscle mass or function to weak or dystrophic muscle.

Panel 2D Summary Ag2452 Highest expression of the NOV3 gene occurs in colon (CT=29.7). High levels of expression are also detectable in breast cancer, prostate cancer, ovarian cancer, and colon cancer when compared to their normal adjacent tissue. Thus, expression of the NOV3 gene could be used as a marker to detect the presence of these cancers.

Panel 4D Summary Ag2002/Ag2452 Two experiments with two different probe and primer sets show highest expression of the NOV3 gene in normal colon (CT=26.2) and dermal fibroblasts treated with TNF-alpha (CT=29.2). Significant expression is also seen in fibroblasts, endothelial and epithelial cells, keratinocytes, leukocytes, smooth muscle cells and normal kidney. The NOV3 gene is expressed at much lower levels in colon from a patient with inflammatory bowel disease (IBD) when compared to expression in normal colon. Similarly, expression in lupus kidney is much lower than normal kidney. Thus, the protein encoded by the NOV3 gene may be involved in normal tissue/cellular functions and at least in the kidney and colon, downregulation of this protein may serve as a diagnostic marker for lupus or IBD.

Panel CNS_neurodegeneration_v1.0 Summary Ag2452 The NOV3 gene is expressed in most of the samples in this panel with highest expression detected in the temporal cortex of a control patient (CT=29.4). While no clear disease association emerged for the gene expression in this neurodegeneration panel, based on its homology to a low density lipoprotein and its expression profile in Panel 1.3D, the NOV3 gene product remains a promising antibody or small molecule target for the treatment of Alzheimer's disease (Caramelli et al., Increased apolipoprotein B serum concentration in Alzheimer's disease. Acta Neurol Scand. 100:61-3, 1999 and Ulery et al., Modulation of beta-amyloid precursor protein processing by the low density lipoprotein receptor-related protein (LRP). Evidence that LRP contributes to the pathogenesis of Alzheimer's disease. J Biol Chem 275(10):7410-5, 2000).

NOV4: Purinoceptor-like

Expression of NOV4 gene (also referred to as AC026756_da1) was assessed using the primer-probe sets Ag1905 and Ag2504 described in Tables 26 and 27. Results from RTQ-PCR runs are shown in Tables 28, 29, and 30.

5 Table 26. Probe Name Ag1905

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-TGAGAATCAGATCCATGAAGCT-3'	58.9	22	1174	114
Probe	TET-5'- CCATTAGCTGCTCTGAACACCTTTGG-3'- TAMRA	67.9	26	1211	115
Reverse	5'-GTCGCTGACCACCACATATAGT-3'	59	22	1246	116

Table 27. Probe Name Ag2504

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CTGAGAGCGAGTTACTGCTCAT-3'	58.9	22	272	117
Probe	TET-5'- TGATTCATATTGCCAACTGAACTCTCTTG -3'-TAMRA	67.1	30	295	118
Reverse	5'-TGTCTCCTTTCATCTTGCAAGA-3'	60	22	328	119

Table 28. Panel 1.3D

Tissue Name	Relative Expression(%)	
	1.3Dtm2783t _ag1905	1.3Dtm2834t _ag1905
Liver adenocarcinoma	0.0	0.0
Pancreas	1.3	3.2
Pancreatic ca. CAPAN 2	0.0	0.0
Adrenal gland	0.0	0.5
Thyroid	1.9	1.1
Salivary gland	2.1	1.2
Pituitary gland	0.0	0.5
Brain (fetal)	2.7	1.3
Brain (whole)	7.5	9.9
Brain (amygdala)	4.2	6.7
Brain (cerebellum)	0.0	0.0
Brain (hippocampus)	4.5	10.7
Brain (substantia nigra)	0.7	0.4
Brain (thalamus)	15.1	9.2
Cerebral Cortex	14.2	17.3
Spinal cord	4.8	1.0
CNS ca (glio/astro) U87-MG	0.0	0.0
CNS ca (glio/astro) U-118-MG	0.4	0.9
CNS ca. (astro) SW1783	0.0	0.4
CNS ca * (neuro. met) SK-N-AS	3.4	1.4

CNS ca. (astro) SF-539	0.0	0.0
CNS ca. (astro) SNB-75	0.0	0.0
CNS ca. (glio) SNB-19	0.0	0.0
CNS ca. (glio) U251	0.0	0.0
CNS ca. (glio) SF-295	0.0	0.0
Heart (fetal)	0.0	0.0
Heart	0.5	0.4
Fetal Skeletal	2.5	3.7
Skeletal muscle	0.0	0.0
Bone marrow	0.4	0.0
Thymus	0.0	0.0
Spleen	0.9	1.6
Lymph node	0.6	1.2
Colorectal	3.5	4.4
Stomach	1.5	1.1
Small intestine	0.3	1.3
Colon ca. SW480	15.2	18.8
Colon ca. * (SW480 met)SW620	5.1	8.8
Colon ca. HT29	0.0	0.0
Colon ca. HCT-116	0.0	0.5
Colon ca. CaCo-2	0.0	1.0
83219 CC Well to Mod Diff (ODO3866)	30.1	38.2
Colon ca. HCC-2998	1.0	0.5
Gastric ca. * (liver met) NCI-N87	0.9	0.0
Bladder	0.0	0.0
Trachea	100.0	61.1
Kidney	5.3	3.7
Kidney (fetal)	1.7	1.9
Renal ca. 786-0	0.0	0.0
Renal ca. A498	0.0	0.0
Renal ca. RXF 393	0.0	0.0
Renal ca. ACHN	0.0	0.0
Renal ca. UO-31	0.0	0.0
Renal ca. TK-10	0.0	0.0
Liver	0.0	0.0
Liver (fetal)	0.0	0.0
Liver ca. (hepatoblast) HepG2	0.0	0.0
Lung	1.9	1.1
Lung (fetal)	3.3	3.8
Lung ca. (small cell) LX-1	3.1	2.1
Lung ca. (small cell) NCI-H69	1.0	0.3
Lung ca. (s cell var.) SHP-77	84.1	100.0
Lung ca. (large cell) NCI-H460	0.0	0.0
Lung ca. (non-sm. cell) A549	0.0	0.0

Table 29. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2Dtm3014t_ag1905		2Dtm3014t_ag1905
Normal Colon GENPAK 061003	21.6	Kidney NAT Clontech 8120608	0.6
83219 CC Well to Mod Diff (ODO3866)	33.9	Kidney Cancer Clontech 8120613	44.1
83220 CC NAT (ODO3866)	7.5	Kidney NAT Clontech 8120614	2.3
83221 CC Gr.2 rectosigmoid (ODO3868)	6.6	Kidney Cancer Clontech 9010320	0.5
83222 CC NAT (ODO3868)	0.3	Kidney NAT Clontech 9010321	2.8
83235 CC Mod Diff (ODO3920)	37.1	Normal Uterus GENPAK 061018	2.2
83236 CC NAT (ODO3920)	2.9	Uterus Cancer GENPAK 064011	8.1
83237 CC Gr 2 ascend colon	100.0	Normal Thyroid Clontech A+	2.3

(ODO3921)		6570-1	
83238 CC NAT (ODO3921)	11.8	Thyroid Cancer GENPAK 064010	0.9
83241 CC from Partial Hepatectomy (ODO4309)	22.2	Thyroid Cancer INVITROGEN A302152	1.0
83242 Liver NAT (ODO4309)	0.0	Thyroid NAT INVITROGEN A302153	2.3
87472 Colon mets to lung (OD04451-01)	12.9	Normal Breast GENPAK 061019	4.5
87473 Lung NAT (OD04451-02)	2.3	84877 Breast Cancer (OD04566)	0.3
Normal Prostate Clontech A+ 6546-1	3.9	85975 Breast Cancer (OD04590-01)	0.0
84140 Prostate Cancer (OD04410)	1.0	85976 Breast Cancer Mets (OD04590-03)	0.6
84141 Prostate NAT (OD04410)	2.5	87070 Breast Cancer Metastasis (OD04655-05)	0.8
87073 Prostate Cancer (OD04720-01)	4.2	GENPAK Breast Cancer 064006	6.9
87074 Prostate NAT (OD04720-02)	4.0	Breast Cancer Res. Gen 1024	14.1
Normal Lung GENPAK 061010	16.6	Breast Cancer Clontech 9100266	1.0
83239 Lung Met to Muscle (ODO4286)	0.0	Breast NAT Clontech 9100265	0.4
83240 Muscle NAT (ODO4286)	0.0	Breast Cancer INVITROGEN A209073	6.7
84136 Lung Malignant Cancer (OD03126)	8.8	Breast NAT INVITROGEN A2090734	11.3
84137 Lung NAT (OD03126)	4.7	Normal Liver GENPAK 061009	0.0
84871 Lung Cancer (OD04404)	3.3	Liver Cancer GENPAK 064003	0.0
84872 Lung NAT (OD04404)	3.9	Liver Cancer Research Genetics RNA 1025	0.5
84875 Lung Cancer (OD04565)	0.0	Liver Cancer Research Genetics RNA 1026	0.0
84876 Lung NAT (OD04565)	0.6	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	0.0
85950 Lung Cancer (OD04237-01)	10.7	Paired Liver Tissue Research Genetics RNA 6004-N	0.6
85970 Lung NAT (OD04237-02)	3.2	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0.6
83255 Ocular Mel Met to Liver (ODO4310)	0.0	Paired Liver Tissue Research Genetics RNA 6005-N	0.0
83256 Liver NAT (ODO4310)	0.5	Normal Bladder GENPAK 061001	0.0
84139 Melanoma Mets to Lung (OD04321)	0.0	Bladder Cancer Research Genetics RNA 1023	0.0
84138 Lung NAT (OD04321)	2.9	Bladder Cancer INVITROGEN A302173	6.3
Normal Kidney GENPAK 061008	66.4	87071 Bladder Cancer (OD04718-01)	2.1
83786 Kidney Ca, Nuclear grade 2 (OD04338)	5.8	87072 Bladder Normal Adjacent (OD04718-03)	2.3
83787 Kidney NAT (OD04338)	49.3	Normal Ovary Res. Gen.	0.0
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.0	Ovarian Cancer GENPAK 064008	16.4
83789 Kidney NAT (OD04339)	28.1	87492 Ovary Cancer (OD04768-07)	0.5
83790 Kidney Ca, Clear cell type	1.5	87493 Ovary NAT (OD04768-08)	0.0

(OD04340)			
83791 Kidney NAT (OD04340)	54.7	Normal Stomach GENPAK 061017	0.5
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.0	Gastric Cancer Clontech 9060358	1.7
83793 Kidney NAT (OD04348)	12.5	NAT Stomach Clontech 9060359	1.4
87474 Kidney Cancer (OD04622-01)	0.0	Gastric Cancer Clontech 9060395	0.5
87475 Kidney NAT (OD04622-03)	1.4	NAT Stomach Clontech 9060394	0.0
85973 Kidney Cancer (OD04450-01)	0.0	Gastric Cancer Clontech 9060397	0.7
85974 Kidney NAT (OD04450-03)	71.2	NAT Stomach Clontech 9060396	0.0
Kidney Cancer Clontech 8120607	0.0	Gastric Cancer GENPAK 064005	1.0

Table 30. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4Dtm3015t_ag1905		4Dtm3015t_ag1905
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	93779_HUVEC (Endothelial)_IFN gamma	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial)_IL-11	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.0	93583_Lung Microvascular Endothelial Cells_none	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium_none	1.3
93570_primary Tr1_anti-CD28/anti-CD3	0.0	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium_none	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92668_Coronary Artery SMC_resting	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107_astrocytes_resting	0.0

ng/ml			
93098_HUVEC (Endothelial)_none	0.0	64030-1_Kidney_none	0.6
93099_HUVEC (Endothelial)_starved	0.0		

Panel 1.3D Summary Ag1905 Two experiments with the same probe and primer set produce results that are in good agreement with highest expression in the lung cancer cell line SHP-77 (CTs=30) and the trachea (CTs=30-31). There is also significant expression of the NOV4 gene in cell lines derived from the colon and ovary. This gene may play a role in different types of lung, ovary and colon cancer as it is more highly expressed in cell lines derived from these cancers compared to the normal tissues. Furthermore, expression in normal brain and pancreas seems to be higher than cancer cell lines derived from these tissues. Thus, expression of the NOV4 gene could be used as a marker or as a therapeutic for colon, ovarian, brain, lung, and pancreatic cancer. In addition, therapeutic modulation of the product of this gene, through the use of peptides, chimeric molecules or small molecule drugs, may be useful in the therapy of these cancers.

There is also significant expression of the NOV4 gene in tissues involved in the central nervous system including the amygdala, hippocampus, thalamus, cerebral cortex, and spinal cord.

Purinoreceptors found in GDNF sensitive sensory neurons mediate nociceptor function. Since the NOV4 gene product is a homolog of a purinoreceptor, agents that block the action of this receptor may have utility in treating pain, either acting as analgesics or inhibiting the establishment of chronic pain. In addition, since adenosine plays a significant neuromodulatory role in brain regions such as the hippocampus, cortex, basal ganglia, and thalamus, the NOV4 purinoreceptor-homolog is localized in a position to participate with the action of adenosine in these brain regions. The protein encoded by the NOV4 gene is most homologous to P2Y4 and P2Y6 purinoreceptors, suggesting that its function may be similar to the PLC-mediated Ca²⁺ mobilization induced by these receptors. Ca²⁺ mobilization is an important component of the molecular process leading to neurotransmitter release. Adenosine modulates the release of glutamate in the brain, which is the main excitatory amino acid neurotransmitter. Glutamate exerts excitotoxic neuronal damage and death in a number of pathological conditions, including stroke. Agonists of A1 adenosine receptors attenuate this damage via G protein-coupled inhibition of glutamate release. Antagonists of A2 receptors also attenuate glutamate induced excitotoxicity. Therefore, agents that inhibit or stimulate the protein encoded by the NOV4 gene are likely to affect glutamate release in the brain and the

subsequent action of glutamate in these regions. If the NOV4 gene product functions similarly to the A1 receptor with respect to glutamate release, then agonists of the putative receptor are likely to have utility in the treatment of stroke. If the NOV4 gene product functions similarly to the A2 receptor, then antagonists of the putative receptor are likely to have utility in the treatment of stroke. Furthermore, antagonists of the A2a purinoceptor are antidepressants. Therefore, antagonists of the NOV4 gene product may be useful antidepressants. A2a receptor antagonists also counter parkinsonian-like symptoms in mice, suggesting that the NOV4 gene product antagonists may also have utility in the treatment of Parkinson's disease.

Ag2504 Expression of the NOV4 gene is low/undetectable (Ct values >35) in all samples in Panel 1.3D (data not shown).

Panel 2.2 Summary Ag2504 Expression of the NOV4 gene is low/undetectable (Ct values >35) in all samples in Panel 2.2 (data not shown).

Panel 2D Summary Ag1905 Highest expression of the NOV4 gene is detected in a colon cancer (CT=30.4). Furthermore, expression of this gene appears to be overexpressed in colon cancer when compared to normal adjacent tissue in all six matched tissue pairs present in this panel. Thus, expression of the AC025756_da1 gene could be used to differentiate between colon cancer and normal tissue. Furthermore, therapeutic modulation of the function or activity of the NOV4 gene product could be effective in the treatment of colon cancer. The NOV4 gene also shows a reverse association in the kidney, with overexpression of the gene present in normal kidney when compared to the corresponding cancerous tissue. Thus, expression of the gene could also be used to differentiate between normal and cancerous kidney tissue and therapeutic modulation of the gene product could be effective in the treatment of renal cancer.

Panel 4D Summary Ag1905 Expression of the NOV4 gene is limited to the thymus (CT=31.9). The putative GPCR encoded by this gene could be important in T cell development since purinoreceptors have been demonstrated in thymocytes. Immunomodulatory, therapeutic drugs designed with the protein encoded for by the NOV4 gene may regulate T cell production in the thymus and be important in preventing tissue rejection, treating autoimmune disorders and treating viral diseases such as AIDS. In addition, the transcript or antibodies designed against the protein encoded for by the transcript could be used as diagnostic markers for identifying subsets of thymocytes at specific developmental stages.

Ag2504 Expression of the NOV4 gene is low/undetectable (Ct values >34.5) in all samples in Panel 4D (data not shown).

Panel CNS_neurodegeneration_v1.0 Summary Ag2504 Expression of the NOV4 gene is low/undetectable (Ct values >35) in all samples in Panel CNS_neurodegeneration_v1.0 (data not shown). (Nagy et al., Apoptosis of murine thymocytes induced by extracellular ATP is dose- and cytosolic pH-dependent. Immunol Lett. 72:23-30, 2000; Liu et al., P2Y purinoceptor activation mobilizes intracellular Ca²⁺ and induces a membrane current in rat intracardiac neurones. J Physiol. 526 Pt 2:287-98, 2000; Ongini et al., Selective adenosine A2A receptor antagonists. Farmaco. 56(1-2):87-90, 2001; Chen et al., Neuroprotection by caffeine and A(2A) adenosine receptor inactivation in a model of Parkinson's disease. J Neurosci. 21:RC143, 2001; Wardas et al., SCH 58261, an A(2A) adenosine receptor antagonist, counteracts parkinsonian-like muscle rigidity in rats. Synapse. 41:160-71, 2001; Driessen et al., Depression of C fiber-evoked activity by intrathecally administered reactive red 2 in rat thalamic neurons. Brain Res. 796 (12):284-90, 1998; El Yacoubi et al., Adenosine A2A receptor antagonists are potential antidepressants: evidence based on pharmacology and A2A receptor knockout mice. Br J Pharmacol. 134:68-77, 2001).

NOV5: CG8841-like

Expression of NOV5 gene (also referred to as AC026756_da1) was assessed using the primer-probe set Ag2000 described in Table 31. Results from RTQ-PCR runs are shown in Tables 32, 33, and 34.

Table 31. Probe Name Ag2000

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-ACTCCACCAAGAAGATCCAGTT-3'	59.1	22	1007	120
Probe	FAM-5'-TCTCTTCTGGAAGCTCTGCGACTTCA-3'-TAMRA	68.8	26	1047	121
Reverse	5'-GCACGAAGAAGAGGAATTTCTT-3'	59	22	1075	122

Table 32. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3Dtm2809f_ag2000		1.3Dtm2809f_ag2000
Liver adenocarcinoma	9.8	Kidney (fetal)	6.0
Pancreas	24.8	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	1.3	Renal ca. A498	1.0
Adrenal gland	3.3	Renal ca. RXF 393	0.0
Thyroid	11.0	Renal ca. ACHN	1.5
Salivary gland	30.6	Renal ca. UO-31	1.1

Pituitary gland	30.4	Renal ca. TK-10	2.4
Brain (fetal)	13.0	Liver	0.7
Brain (whole)	39.2	Liver (fetal)	2.5
Brain (amygdala)	23.7	Liver ca. (hepatoblast) HepG2	8.8
Brain (cerebellum)	21.0	Lung	12.9
Brain (hippocampus)	46.7	Lung (fetal)	30.4
Brain (substantia nigra)	10.4	Lung ca. (small cell) LX-1	8.7
Brain (thalamus)	33.2	Lung ca. (small cell) NCI-H69	29.5
Cerebral Cortex	100.0	Lung ca. (s.cell var.) SHP-77	33.0
Spinal cord	14.6	Lung ca. (large cell) NCI-H460	0.9
CNS ca. (glio/astro) U87-MG	0.1	Lung ca. (non-sm. cell) A549	15.9
CNS ca. (glio/astro) U-118-MG	0.3	Lung ca. (non-s.cell) NCI-H23	2.3
CNS ca. (astro) SW1783	0.0	Lung ca (non-s cell) HOP-62	3.3
CNS ca.* (neuro; met) SK-N-AS	4.3	Lung ca. (non-s.cl) NCI-H522	1.8
CNS ca. (astro) SF-539	0.0	Lung ca. (squamous) SW 900	20.2
CNS ca. (astro) SNB-75	35.6	Lung ca. (squamous) NCI-H596	3.3
CNS ca. (glio) SNB-19	5.7	Mammary gland	40.1
CNS ca. (glio) U251	2.1	Breast ca.* (pl. effusion) MCF-7	42.0
CNS ca. (glio) SF-295	2.6	Breast ca.* (pl.ef) MDA-MB-231	6.3
Heart (fetal)	44.4	Breast ca.* (pl. effusion) T47D	73.2
Heart	3.6	Breast ca. BT-549	0.0
Fetal Skeletal	69.3	Breast ca. MDA-N	0.2
Skeletal muscle	0.6	Ovary	17.6
Bone marrow	1.8	Ovarian ca. OVCAR-3	23.5
Thymus	2.9	Ovarian ca. OVCAR-4	9.2
Spleen	14.8	Ovarian ca. OVCAR-5	13.0
Lymph node	8.6	Ovarian ca. OVCAR-8	2.8
Colorectal	18.9	Ovarian ca. IGROV-1	1.9
Stomach	68.3	Ovarian ca.* (ascites) SK-OV-3	2.7
Small intestine	21.9	Uterus	9.9
Colon ca. SW480	10.0	Placenta	27.2
Colon ca.* (SW480 met)SW620	2.9	Prostate	25.9
Colon ca. HT29	16.8	Prostate ca.* (bone met)PC-3	18.7
Colon ca. HCT-116	5.5	Testis	7.4
Colon ca. CaCo-2	11.6	Melanoma Hs688(A).T	0.0
83219 CC Well to Mod Diff (ODO3866)	27.0	Melanoma* (met) Hs688(B) T	0.1
Colon ca. HCC-2998	17.2	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	48.6	Melanoma M14	0.0
Bladder	10.7	Melanoma LOX IMVI	0.0
Trachea	36.1	Melanoma* (met) SK-MEL-5	0.7
Kidney	1.9	Adipose	4.3

Table 33. Panel 2.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2.2x4tm6394 f_ag2000_a1		2.2x4tm6394 f_ag2000_a1
Normal Colon GENPAK 061003	13.9	83793 Kidney NAT (OD04348)	10.7
97759 Colon cancer (OD06064)	21.3	98938 Kidney malignant cancer (OD06204B)	29.6
97760 Colon cancer NAT (OD06064)	24.4	98939 Kidney normal adjacent tissue (OD06204E)	3.8
97778 Colon cancer (OD06159)	7.0	85973 Kidney Cancer (OD04450-01)	4.1
97779 Colon cancer NAT (OD06159)	11.0	85974 Kidney NAT (OD04450-03)	5.0
98861 Colon cancer (OD06297-04)	8.7	Kidney Cancer Clontech 8120613	1.3
98862 Colon cancer NAT (OD06297-015)	14.1	Kidney NAT Clontech 8120614	7.6
83237 CC Gr.2 ascend colon (ODO3921)	9.4	Kidney Cancer Clontech 9010320	2.7
83238 CC NAT (ODO3921)	4.8	Kidney NAT Clontech 9010321	2.9
97766 Colon cancer metastasis (OD06104)	3.2	Kidney Cancer Clontech 8120607	8.9
97767 Lung NAT (OD06104)	10.2	Kidney NAT Clontech 8120608	3.0
87472 Colon mets to lung (OD04451-01)	10.8	Normal Uterus GENPAK 061018	9.0
87473 Lung NAT (OD04451-02)	8.3	Uterus Cancer GENPAK 064011	4.9
Normal Prostate Clontech A+ 6546-1 (8090438)	43.0	Normal Thyroid Clontech A+ 6570-1 (7080817)	5.4
84140 Prostate Cancer (OD04410)	17.2	Thyroid Cancer GENPAK 064010	2.8
84141 Prostate NAT (OD04410)	10.4	Thyroid Cancer INVITROGEN A302152	6.3
Normal Ovary Res. Gen.	7.6	Thyroid NAT INVITROGEN A302153	4.6
98863 Ovarian cancer (OD06283-03)	9.5	Normal Breast GENPAK 061019	19.6
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	4.7	84877 Breast Cancer (OD04566)	15.8
Ovarian Cancer GENPAK 064008	7.3	Breast Cancer Res. Gen. 1024	22.3
97773 Ovarian cancer (OD06145)	0.4	85975 Breast Cancer (OD04590-01)	47.6
97775 Ovarian cancer NAT (OD06145)	7.3	85976 Breast Cancer Mets (OD04590-03)	41.3
98853 Ovarian cancer (OD06455-03)	18.0	87070 Breast Cancer Metastasis (OD04655-05)	100.0
98854 Ovarian NAT (OD06455-07) Fallopian tube	2.4	GENPAK Breast Cancer 064006	11.1
Normal Lung GENPAK 061010	18.6	Breast Cancer Clontech 9100266	49.1
92337 Invasive poor diff. lung adeno (ODO4945-01)	10.0	Breast NAT Clontech 9100265	20.7
92338 Lung NAT (ODO4945-03)	5.7	Breast Cancer INVITROGEN A209073	18.6
84136 Lung Malignant Cancer (OD03126)	17.6	Breast NAT INVITROGEN A2090734	21.5
84137 Lung NAT (OD03126)	3.9	97763 Breast cancer (OD06083)	81.2
90372 Lung Cancer (OD05014A)	11.4	97764 Breast cancer node metastasis (OD06083)	65.8

90373 Lung NAT (OD05014B)	0.2	Normal Liver GENPAK 061009	2 4
97761 Lung cancer (OD06081)	4.2	Liver Cancer Research Genetics RNA 1026	4.4
97762 Lung cancer NAT (OD06081)	6 2	Liver Cancer Research Genetics RNA 1025	4.6
85950 Lung Cancer (OD04237-01)	4 6	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	3.8
85970 Lung NAT (OD04237-02)	9.1	Paired Liver Tissue Research Genetics RNA 6004-N	1.5
83255 Ocular Mel Met to Liver (ODO4310)	0.7	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	12.1
83256 Liver NAT (ODO4310)	2.8	Paired Liver Tissue Research Genetics RNA 6005-N	9.6
84139 Melanoma Mets to Lung (OD04321)	0.3	Liver Cancer GENPAK 064003	1.5
84138 Lung NAT (OD04321)	9 2	Normal Bladder GENPAK 061001	19 6
Normal Kidney GENPAK 061008	2.4	Bladder Cancer Research Genetics RNA 1023	6.3
83786 Kidney Ca, Nuclear grade 2 (OD04338)	9.7	Bladder Cancer INVITROGEN A302173	8 6
83787 Kidney NAT (OD04338)	1.7	Normal Stomach GENPAK 061017	62 5
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	4.2	Gastric Cancer Clontech 9060397	5 1
83789 Kidney NAT (OD04339)	4.1	NAT Stomach Clontech 9060396	38.5
83790 Kidney Ca, Clear cell type (OD04340)	2.7	Gastric Cancer Clontech 9060395	21 5
83791 Kidney NAT (OD04340)	6.7	NAT Stomach Clontech 9060394	43 5
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.6	Gastric Cancer GENPAK 064005	11 4

Table 34. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4dx4tm5534f_ag2000_a1		4dx4tm5534f_ag2000_a1
93768_Secondary Th1_anti-CD28/anti-CD3	0.2	93100_HUVEC (Endothelial)_IL-1b	4 8
93769_Secondary Th2_anti-CD28/anti-CD3	0.3	93779_HUVEC (Endothelial)_IFN gamma	14 7
93770_Secondary Tr1_anti-CD28/anti-CD3	0.6	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	1 9
93573_Secondary Th1_resting day 4-6 in IL-2	0.1	93101_HUVEC (Endothelial)_TNF alpha + IL4	4 0
93572_Secondary Th2_resting day 4-6 in IL-2	0.7	93781_HUVEC (Endothelial)_IL-11	15 7
93571_Secondary Tr1_resting day 4-6 in IL-2	0.3	93583_Lung Microvascular Endothelial Cells_none	14 4
93568_primary Th1_anti-CD28/anti-CD3	0.1	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	6 3
93569_primary Th2_anti-CD28/anti-CD3	0 2	92662_Microvascular Dermal endothelium_none	15 5
93570_primary Tr1_anti-	0.1	92663_Microvascular Dermal	5 2

CD28/anti-CD3		endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	
93565_primary Th1_resting dy 4-6 in IL-2	0.4	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	2.6
93566_primary Th2_resting dy 4-6 in IL-2	0.2	93347_Small Airway Epithelium_none	0.8
93567_primary Tr1_resting dy 4-6 in IL-2	0.1	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	3.4
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.3	92668_Coronary Artery SMC_resting	0.1
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.7	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.3
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.8	93107_astrocytes_resting	3.6
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.9	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	6.9
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	92666_KU-812 (Basophil)_resting	0.0
93354_CD4_none	2.7	92667_KU-812 (Basophil)_PMA/ionomycin	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.0	93579_CCD1106 (Keratinocytes)_none	0.3
93103_LAK cells_resting	1.5	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	1.5
93788_LAK cells_IL-2	2.6	93791_Liver Cirrhosis	11.3
93787_LAK cells_IL-2+IL-12	1.4	93792_Lupus Kidney	9.2
93789_LAK cells_IL-2+IFN gamma	1.2	93577_NCI-H292	20.3
93790_LAK cells_IL-2+ IL-18	1.6	93358_NCI-H292_IL-4	17.5
93104_LAK cells_PMA/ionomycin and IL-18	0.3	93360_NCI-H292_IL-9	21.6
93578_NK Cells_IL-2_resting	0.4	93359_NCI-H292_IL-13	9.5
93109_Mixed Lymphocyte Reaction_Two Way MLR	1.2	93357_NCI-H292_IFN gamma	10.3
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.4	93777_HPAEC_-	13.7
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC_IL-1 beta/TNA alpha	9.2
93112_Mononuclear Cells (PBMcs)_resting	0.8	93254_Normal Human Lung Fibroblast_none	0.2
93113_Mononuclear Cells (PBMcs)_PWM	0.2	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.8
93114_Mononuclear Cells (PBMcs)_PHA-L	0.3	93257_Normal Human Lung Fibroblast_IL-4	0.1
93249_Ramos (B cell)_none	0.5	93256_Normal Human Lung Fibroblast_IL-9	0.2
93250_Ramos (B cell)_ionomycin	0.7	93255_Normal Human Lung Fibroblast_IL-13	0.2
93349_B lymphocytes_PWM	0.8	93258_Normal Human Lung Fibroblast_IFN gamma	0.3
93350_B lymphocytes_CD40L and IL-4	5.8	93106_Dermal Fibroblasts CCD1070_resting	0.1

92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionom ycin	0.0	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.1
93356_Dendritic Cells_none	0.2	93772_dermal fibroblast_IFN gamma	0.1
93355_Dendritic Cells_LPS 100 ng/ml	0.0	93771_dermal fibroblast_IL-4	0.1
93775_Dendritic Cells_anti-CD40	0.0	93260_IBD Colitis 2	2.9
93774_Monocytes_resting	0.0	93261_IBD Crohns	9.3
93776_Monocytes_LPS 50 ng/ml	0.0	735010_Colon_normal	100.0
93581_Macrophages_resting	0.1	735019_Lung_none	19.4
93582_Macrophages_LPS 100 ng/ml	0.0	64028-1_Thymus_none	11.2
93098_HUVEC (Endothelial)_none	7.4	64030-1_Kidney_none	6.4
93099_HUVEC (Endothelial)_starved	17.8		

Panel 1.3D Summary Highest expression of the NOV5 gene, a homolog of a transmembrane multi-pass protein, is seen in the cerebral cortex (CT=26.8), with moderate expression detectable across all regions of the brain. Because this gene shows a large down-regulation in brain cancers, its absence would be an excellent marker to determine if brain tissue was pre-cancerous in the examining and classifying of postmortem tissue

Expression of the NOV5 gene is also widespread among tissues with metabolic relevance, including adipose, pancreas, adult and fetal heart, adult and fetal liver, adult and fetal skeletal muscle, and the adrenal, pituitary, and thyroid glands. The NOV5 gene is expressed at much higher levels in fetal heart and skeletal muscle (CTs=28) than in adult heart and skeletal muscle (CTs=31-34). This differential expression pattern suggests that NOV5 gene expression could be used to differentiate between the two tissue sources for heart and skeletal muscle. Furthermore, the significantly higher level of expression of the gene in fetal skeletal muscle suggests that the NOV5 gene product may be involved in muscular growth or development in the fetus and could potentially act in a regenerative capacity in an adult. Therefore, therapeutic modulation of the NOV5 gene could be useful in the treatment of muscle related diseases and the treatment of weak or dystrophic muscle.

The NOV5 gene is also expressed at significant levels in cell lines derived from ovarian, breast, lung, gastric, prostate and colon cancers compared to the normal tissues. Thus, the expression of this gene could be of use as a marker or as a therapeutic for ovarian, breast, lung, gastric, prostate and colon. In addition, therapeutic modulation of the product of this

gene, through the use of peptides, chimeric molecules or small molecule drugs, may be useful in the treatment of these cancers.

Panel 2.2 Summary Highest expression of the NOV5 gene is seen in breast cancer (CT=28) as is seen in Panel 1.3D. In addition, there is significant overexpression of the NOV5 gene in a cluster of breast, lung, and ovarian cancer samples when compared to corresponding normal tissues. Thus, expression of the NOV5 gene could be used to differentiate breast, ovarian and lung cancers from normal tissue and as a marker for the presence of these cancers. Furthermore, therapeutic modulation of the protein product of the NOV5 gene could be beneficial in the treatment of breast, ovarian and lung cancers. The expression of this gene also shows a reverse association with some normal stomach samples when compared to the matched gastric cancer tissue. This suggests that the NOV5 gene could be used to distinguish between normal and cancerous gastric tissue and that therapeutic modulation of the gene product may be useful in the treatment of gastric cancer.

Panel 4D Summary The highest expression of the NOV5 gene is found in the colon (CT=26.2), with modest expression detectable in the muco-epidermoid cell line H292, and the lung. It is also expressed at moderate levels on HUVEC and lung microvasculature regardless of their activation status. The protein encoded by the NOV5 gene is homologous to an epidermal growth factor related protein (fibropellin like) and could be used as a marker of lung muco-epidermoid cells, colon or vasculature. The putative protein encoded by the transcript may also play an important role in the normal homeostasis of these tissues. Small molecule or antibody therapeutics designed with the NOV5 gene product could be important for maintaining or restoring normal function to these organs during inflammation associated with asthma and emphysema.

NOV6: Synaptotagmin-like

Expression of NOV6 gene (also referred to as SC134912642_da1) was assessed using the primer-probe set Ag2056 described in Table 35. Results from RTQ-PCR runs are shown in Tables 36, 37, 38, 39 and 40.

Table 35. Probe Name Ag2056

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CTGGTCTCTGCCATCATCAC-3'	59.2	20	55	123
Probe	TET-5'-CTTAGCGTCACTGTCGTCCTCGCTAG-3'-TAMRA	68.4	26	82	124
Reverse	5'-TGTAGCGTTTGCCAGTTT-3'	59.3	19	130	125

Table 36. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3Dtm2580t _ag2056		1.3Dtm2580t _ag2056
Liver adenocarcinoma	2.4	Kidney (fetal)	1.9
Pancreas	1.8	Renal ca. 786-0	0.2
Pancreatic ca. CAPAN 2	2.3	Renal ca. A498	6.0
Adrenal gland	0.8	Renal ca. RXF 393	0.8
Thyroid	1.3	Renal ca. ACHN	0.0
Salivary gland	7.9	Renal ca. UO-31	0.0
Pituitary gland	16.3	Renal ca. TK-10	0.6
Brain (fetal)	4.8	Liver	0.3
Brain (whole)	26.8	Liver (fetal)	1.1
Brain (amygdala)	24.0	Liver ca. (hepatoblast) HepG2	1.8
Brain (cerebellum)	8.8	Lung	0.6
Brain (hippocampus)	56.3	Lung (fetal)	0.9
Brain (substantia nigra)	2.9	Lung ca. (small cell) LX-1	7.3
Brain (thalamus)	23.0	Lung ca. (small cell) NCI-H69	16.2
Cerebral Cortex	100.0	Lung ca. (s.cell var.) SHP-77	20.6
Spinal cord	0.6	Lung ca. (large cell) NCI-H460	0.1
CNS ca. (glio/astro) U87-MG	0.4	Lung ca. (non-sm. cell) A549	0.1
CNS ca. (glio/astro) U-118-MG	19.1	Lung ca. (non-s.cell) NCI-H23	0.6
CNS ca. (astro) SW1783	1.8	Lung ca. (non-s.cell) HOP-62	0.3
CNS ca.* (neuro; met) SK-N-AS	0.6	Lung ca. (non-s.cl) NCI-H522	2.0
CNS ca. (astro) SF-539	0.5	Lung ca. (squamous) SW 900	1.1
CNS ca. (astro) SNB-75	17.0	Lung ca. (squamous) NCI-H596	13.3
CNS ca. (glio) SNB-19	0.0	Mammary gland	12.9
CNS ca. (glio) U251	0.1	Breast ca.* (pl. effusion) MCF-7	4.7
CNS ca. (glio) SF-295	0.6	Breast ca.* (pl.ef) MDA-MB-231	0.1
Heart (fetal)	2.8	Breast ca.* (pl. effusion) T47D	17.1
Heart	1.7	Breast ca. BT-549	0.0
Fetal Skeletal	9.4	Breast ca. MDA-N	0.1
Skeletal muscle	0.1	Ovary	0.9
Bone marrow	0.0	Ovarian ca. OVCAR-3	2.5
Thymus	0.1	Ovarian ca. OVCAR-4	1.1
Spleen	1.1	Ovarian ca. OVCAR-5	3.9
Lymph node	0.1	Ovarian ca. OVCAR-8	2.3
Colorectal	3.2	Ovarian ca. IGROV-1	0.0
Stomach	1.9	Ovarian ca.* (ascites) SK-OV-3	3.5
Small intestine	0.3	Uterus	1.3
Colon ca. SW480	6.7	Placenta	18.0
Colon ca.* (SW480 met)SW620	0.3	Prostate	18.8
Colon ca. HT29	1.5	Prostate ca.* (bone met)PC-3	4.5
Colon ca. HCT-116	4.5	Testis	2.3

Colon ca. CaCo-2	18.8	Melanoma Hs688(A).T	0.0
83219 CC Well to Mod Diff (ODO3866)	14.7	Melanoma* (met) Hs688(B) T	1.6
Colon ca. HCC-2998	10.6	Melanoma UACC-62	0.1
Gastric ca.* (liver met) NCI-N87	10.5	Melanoma M14	0.0
Bladder	0.9	Melanoma LOX IMVI	0.6
Trachea	3.5	Melanoma* (met) SK-MEL-5	1.5
Kidney	0.5	Adipose	1.0

Table 37. Panel 2.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2.2x4tm6379 t_ag2056_a1		2.2x4tm6379 t_ag2056_a1
Normal Colon GENPAK 061003	5.3	83793 Kidney NAT (OD04348)	10.3
97759 Colon cancer (OD06064)	0.0	98938 Kidney malignant cancer (OD06204B)	1.3
97760 Colon cancer NAT (OD06064)	0.7	98939 Kidney normal adjacent tissue (OD06204E)	0.8
97778 Colon cancer (OD06159)	1.1	85973 Kidney Cancer (OD04450- 01)	0.0
97779 Colon cancer NAT (OD06159)	1.7	85974 Kidney NAT (OD04450-03)	2.7
98861 Colon cancer (OD06297-04)	2.9	Kidney Cancer Clontech 8120613	2.1
98862 Colon cancer NAT (OD06297-015)	4.2	Kidney NAT Clontech 8120614	3.0
83237 CC Gr.2 ascend colon (ODO3921)	2.3	Kidney Cancer Clontech 9010320	0.2
83238 CC NAT (ODO3921)	1.3	Kidney NAT Clontech 9010321	0.6
97766 Colon cancer metastasis (OD06104)	0.0	Kidney Cancer Clontech 8120607	0.5
97767 Lung NAT (OD06104)	0.0	Kidney NAT Clontech 8120608	1.3
87472 Colon mets to lung (OD04451-01)	4.1	Normal Uterus GENPAK 061018	1.0
87473 Lung NAT (OD04451-02)	0.0	Uterus Cancer GENPAK 064011	0.6
Normal Prostate Clontech A+ 6546-1 (8090438)	11.8	Normal Thyroid Clontech A+ 6570-1 (7080817)	0.0
84140 Prostate Cancer (OD04410)	14.1	Thyroid Cancer GENPAK 064010	0.0
84141 Prostate NAT (OD04410)	21.1	Thyroid Cancer INVITROGEN A302152	1.4
Normal Ovary Res. Gen.	0.0	Thyroid NAT INVITROGEN A302153	0.3
98863 Ovarian cancer (OD06283- 03)	0.3	Normal Breast GENPAK 061019	2.9
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	0.3	84877 Breast Cancer (OD04566)	2.0
Ovarian Cancer GENPAK 064008	0.6	Breast Cancer Res. Gen. 1024	8.5
97773 Ovarian cancer (OD06145)	0.2	85975 Breast Cancer (OD04590- 01)	39.2
97775 Ovarian cancer NAT (OD06145)	0.8	85976 Breast Cancer Mets (OD04590-03)	22.1
98853 Ovarian cancer (OD06455-)	3.5	87070 Breast Cancer Metastasis	100.0

03)		(OD04655-05)	
98854 Ovarian NAT (OD06455-07) Fallopian tube	0.3	GENPAK Breast Cancer 064006	5.7
Normal Lung GENPAK 061010	0.2	Breast Cancer Clontech 9100266	3.6
92337 Invasive poor diff. lung adeno (ODO4945-01)	1.3	Breast NAT Clontech 9100265	5.5
92338 Lung NAT (ODO4945-03)	0.4	Breast Cancer INVITROGEN A209073	1.6
84136 Lung Malignant Cancer (OD03126)	6.9	Breast NAT INVITROGEN A2090734	5.5
84137 Lung NAT (OD03126)	0.0	97763 Breast cancer (OD06083)	5.0
		97764 Breast cancer node metastasis (OD06083)	11.7
90372 Lung Cancer (OD05014A)	4.6	Normal Liver GENPAK 061009	2.5
90373 Lung NAT (OD05014B)	0.7	Liver Cancer Research Genetics RNA 1026	0.8
97761 Lung cancer (OD06081)	1.0	Liver Cancer Research Genetics RNA 1025	2.7
97762 Lung cancer NAT (OD06081)	0.0	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	2.0
85950 Lung Cancer (OD04237-01)	0.7	Paired Liver Tissue Research Genetics RNA 6004-N	2.0
85970 Lung NAT (OD04237-02)	0.3	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	1.1
83255 Ocular Mel Met to Liver (ODO4310)	3.7	Paired Liver Tissue Research Genetics RNA 6005-N	0.5
83256 Liver NAT (ODO4310)	0.5		
84139 Melanoma Mets to Lung (OD04321)	0.0	Liver Cancer GENPAK 064003	0.4
84138 Lung NAT (OD04321)	0.5	Normal Bladder GENPAK 061001	1.4
Normal Kidney GENPAK 061008	0.8	Bladder Cancer Research Genetics RNA 1023	0.5
83786 Kidney Ca, Nuclear grade 2 (OD04338)	9.6	Bladder Cancer INVITROGEN A302173	0.9
83787 Kidney NAT (OD04338)	0.3	Normal Stomach GENPAK 061017	0.6
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.0	Gastric Cancer Clontech 9060397	2.0
83789 Kidney NAT (OD04339)	0.9	NAT Stomach Clontech 9060396	0.0
83790 Kidney Ca, Clear cell type (OD04340)	0.0	Gastric Cancer Clontech 9060395	0.2
83791 Kidney NAT (OD04340)	1.2	NAT Stomach Clontech 9060394	2.3
83792 Kidney Ca, Nuclear grade 3 (OD04348)	1.1	Gastric Cancer GENPAK 064005	1.4

Tissue Name	Relative Expression(%)	
	4dx4tm4455t _ag2056_a1	4dx4tm4982t _ag2056_a1
93768_Secondary Th1 anti-CD28/anti-CD3	0.0	0.0
93769_Secondary Th2 anti-CD28/anti-CD3	0.3	0.5
93770_Secondary Tr1 anti-CD28/anti-CD3	0.0	0.0
93573_Secondary Th1 resting day 4-6 in IL-2	0.0	0.0

93572_Secondary Th2_resting day 4-6 in IL-2	0 0	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0 0	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.4	0.0
93569_primary Th2_anti-CD28/anti-CD3	0 0	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0 4	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0 0	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0 0	0.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.4
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0 0	0.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.3	0.7
93354_CD4_none	0.0	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0 0	0.0
93103_LAK cells_resting	0 4	1.7
93788_LAK cells_IL-2	0.0	0.0
93787_LAK cells_IL-2+IL-12	0.3	0.0
93789_LAK cells_IL-2+IFN gamma	0.4	0.0
93790_LAK cells_IL-2+ IL-18	0.0	0.0
93104_LAK cells_PMA/ionomycin and IL-18	0.2	0.3
93578_NK Cells IL-2_resting	0.0	0.0
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.3	0.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.5	1.7
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.4	0.6
93112_Mononuclear Cells (PBMCs)_resting	0.4	0.0
93113_Mononuclear Cells (PBMCs)_PWM	0.0	0.0
93114_Mononuclear Cells (PBMCs)_PHA-L	0 0	0.0
93249_Ramos (B cell)_none	0.0	0.0
93250_Ramos (B cell)_ionomycin	0.0	0.0
93349_B lymphocytes_PWM	0.0	0.0
93350_B lymphocytes_CD40L and IL-4	0 0	0.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	0.0
93356_Dendritic Cells_none	0.0	0.6
93355_Dendritic Cells_LPS 100 ng/ml	0.3	0.7
93775_Dendritic Cells_anti-CD40	0.0	0 0
93774_Monocytes_resting	0.0	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	0.0
93581_Macrophages_resting	1.1	0.6
93582_Macrophages_LPS 100 ng/ml	4.8	4 4
93098_HUVEC (Endothelial)_none	0.0	0.0
93099_HUVEC (Endothelial)_starved	0.0	0.7
93100_HUVEC (Endothelial)_IL-1b	0.0	0 0

93779_HUVEC (Endothelial)_ IFN gamma	0.0	0.5
93102_HUVEC (Endothelial)_ TNF alpha + IFN gamma	0.0	0.0
93101_HUVEC (Endothelial)_ TNF alpha + IL4	0.0	0.0
93781_HUVEC (Endothelial)_ IL-11	0.8	0.5
93583_Lung Microvascular Endothelial Cells_ none	0.0	0.0
93584_Lung Microvascular Endothelial Cells_ TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
92662_Microvascular Dermal endothelium_ none	0.7	0.0
92663_Microvascular Dermal endothelium_ TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.4	0.0
93773_Bronchial epithelium_ TNFa (4 ng/ml) and IL1b (1 ng/ml) **	4.3	44.0
93347_Small Airway Epithelium_ none	1.6	6.1
93348_Small Airway Epithelium_ TNFa (4 ng/ml) and IL1b (1 ng/ml)	17.8	18.0
92668_Coronary Artery SMC_ resting	0.0	1.3
92669_Coronary Artery SMC_ TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.0	1.1
93107_astrocytes_ resting	0.0	0.0
93108_astrocytes_ TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.4	0.0
92666_KU-812 (Basophil)_ resting	0.8	0.4
92667_KU-812 (Basophil)_ PMA/ionoycin	0.4	1.1
93579_CCD1106 (Keratinocytes)_ none	6.4	9.7
93580_CCD1106 (Keratinocytes)_ TNFa and iFNg **	0.0	13.3
93791_Liver Cirrhosis	0.1	1.4
93792_Lupus Kidney	1.6	1.7
93577_NCI-H292	37.5	35.2
93358_NCI-H292_IL-4	19.8	19.1
93360_NCI-H292_IL-9	31.1	31.3
93359_NCI-H292_IL-13	8.6	9.7
93357_NCI-H292_IFN gamma	9.6	10.7
93777_HPAEC_ -	0.0	0.0
93778_HPAEC_IL-1 beta/TNA alpha	0.0	0.0
93254_Normal Human Lung Fibroblast_ none	33.5	41.6
93253_Normal Human Lung Fibroblast_ TNFa (4 ng/ml) and IL-1b (1 ng/ml)	16.3	25.0
93257_Normal Human Lung Fibroblast_IL-4	77.1	77.1
93256_Normal Human Lung Fibroblast_IL-9	59.5	68.4
93255_Normal Human Lung Fibroblast_IL-13	51.1	69.2
93258_Normal Human Lung Fibroblast_IFN gamma	100.0	100.0
93106_Dermal Fibroblasts CCD1070_ resting	0.0	1.4
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.0	0.0
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0	1.4
93772_dermal fibroblast_IFN gamma	8.7	8.4
93771_dermal fibroblast_IL-4	16.4	25.3
93260_IBD Colitis 2	0.8	0.0
93261_IBD Crohns	2.1	0.0
735010_Colon_ normal	11.9	13.2
735019_Lung_ none	8.1	5.2

102651_BA17 Parkinson's	64.3	102669_Cing Gyr Huntington's	35.6
102658_BA17 Parkinson's2	100.0	102676_Cing Gyr Huntington's2	17.3
102666_BA17 Huntington's	53.9	102608_Cing Gyr PSP	12.4
102673_BA17 Huntington's2	22.0	102616_Cing Gyr PSP2	3.9
102590_BA17 Depression	9.8	102594_Cing Gyr Depression	10.5
102597_BA17 Depression2	40.5	102601_Cing Gyr Depression2	13.9

Table 40. Panel CNS_neurodegeneration_v1.0

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm7005t_ag2056_b1_s2		tm7005t_ag2056_b1_s2
AD 1 Hippo	9.7	Control (Path) 3 Temporal Ctx	2.6
AD 2 Hippo	19.2	Control (Path) 4 Temporal Ctx	31.2
AD 3 Hippo	3.8	AD 1 Occipital Ctx	9.8
AD 4 Hippo	6.1	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	3.6
AD 6 Hippo	26.9	AD 4 Occipital Ctx	12.5
Control 2 Hippo	14.3	AD 5 Occipital Ctx	11.1
Control 4 Hippo	4.7	AD 6 Occipital Ctx	27.6
Control (Path) 3 Hippo	3.2	Control 1 Occipital Ctx	1.4
AD 1 Temporal Ctx	6.6	Control 2 Occipital Ctx	44.9
AD 2 Temporal Ctx	23.5	Control 3 Occipital Ctx	19.6
AD 3 Temporal Ctx	9.0	Control 4 Occipital Ctx	3.6
AD 4 Temporal Ctx	19.4	Control (Path) 1 Occipital Ctx	62.4
AD 5 Inf Temporal Ctx	74.9	Control (Path) 2 Occipital Ctx	16.9
AD 5 Sup Temporal Ctx	38.2	Control (Path) 3 Occipital Ctx	1.4
AD 6 Inf Temporal Ctx	28.5	Control (Path) 4 Occipital Ctx	24.9
AD 6 Sup Temporal Ctx	26.6	Control 1 Parietal Ctx	4.8
Control 1 Temporal Ctx	3.7	Control 2 Parietal Ctx	29.0
Control 2 Temporal Ctx	24.9	Control 3 Parietal Ctx	16.5
Control 3 Temporal Ctx	10.4	Control (Path) 1 Parietal Ctx	54.5
Control 4 Temporal Ctx	9.7	Control (Path) 2 Parietal Ctx	14.2
Control (Path) 1 Temporal Ctx	37.8	Control (Path) 3 Parietal Ctx	2.3
Control (Path) 2 Temporal Ctx	27.2	Control (Path) 4 Parietal Ctx	45.9

- Panel 1.3D Summary** The NOV6 gene is a homolog of synaptotagmin, and shows moderate to high expression across all brain regions with highest expression in the cerebral cortex (CT = 27.6) Synaptotagmin is a presynaptic protein involved in synaptic vesicle release, making this an ideal drug target for diseases such as epilepsy, in which reduction of neurotransmission is beneficial. Selective inhibition of this gene or its protein product may therefore be useful in the treatment of seizure disorders. Furthermore, selective inhibition of

neural transmission through antagonism of the protein encoded by the NOV6 gene may show therapeutic benefit in psychiatric diseases where it is believed that inappropriate neural connections have been established, such as schizophrenia and bipolar disorder. In addition, antibodies against synaptotagmin may cause Lambert-Eaton myasthenic syndrome. Therefore, peptide fragments of the protein encoded by the NOV6 gene may serve to block the action of these antibodies and treat Lambert-Eaton myasthenic syndrome.

The NOV6 gene also shows low but significant expression in many metabolic tissues including adipose, adult and fetal heart, adult and fetal liver, pancreas, and the adrenal, pituitary and thyroid glands. This gene product appears to be expressed at much higher levels in fetal skeletal muscle (CT value = 31) when compared to adult skeletal muscle (CT value = 37), and may be useful for the differentiation of the adult from the fetal phenotype in this tissue.

The NOV6 gene is significantly expressed in a cluster of cell lines derived from lung, gastric, colon and ovarian cancer compared to the normal tissues. The expression of this gene also shows an association with some normal brain and prostate samples when compared to the cell lines derived from cancers of these tissues. Thus, based upon its profile, the expression of this gene could be of use as a marker or as a therapeutic for lung, gastric, colon and ovarian cancers. In addition, therapeutic modulation of the product of this gene, through the use of peptides, antibodies, chimeric molecules or small molecule drugs, may be useful in the treatment of these cancers.

Panel 2.2 Summary Expression of the NOV6 gene is highest in a breast cancer metastasis (CT=27.8) and appears to be highly expressed in samples derived from breast cancer when compared to normal adjacent tissue. The expression of this gene also shows an association with some normal kidney, prostate and lung samples when compared to the matched kidney, prostate and lung cancer tissue. Thus, based upon its profile, absence/presence of expression of this gene could be of use as a marker for breast, kidney, prostate and lung cancer. Therapeutic modulation of the product of this gene, through the use of peptides, antibodies, chimeric molecules or small molecule drugs, may be useful in the therapy of lung, kidney, prostate and breast cancers.

Panel 4D Summary Results from two experiments with the same probe and primer set show that the NOV6 gene is selectively expressed, at moderate levels, in lung related tissues. Expression of the gene is found on normal human lung fibroblast and is up regulated in these cells following treatment with IFN γ , IL4, IL13 and IL-9, with highest expression in IFN γ treated cells (CTs=30). The protein encoded by the NOV6 gene is also up regulated in small

airway epithelium treated with TNF- α and IL-1 β and downregulated in the muco-epidermoid cell line H292 upon treatment with IL-13 and IFN γ . The NOV6 gene is a homolog of synaptotagmin, whose ubiquitously expressed isoform, synaptotagmin VII, regulates exocytosis of lysosomes. Synaptotagmin VII has recently been implicated in fibroblast plasma membrane repair along with lysosomes which act as Ca(2+)-regulated exocytic compartments responsible for the plasma membrane repair. Therefore, therapeutic modulation of the expression or function of this gene or gene product, through the use of antibodies or small molecule drugs, might be beneficial for treating lung diseases such as asthma, emphysema, and viral and bacterial lung infection associated with cellular stress due to the local production of inflammatory cytokines.

Panel CNS_1 Summary Highest expression of the NOV6 gene is seen in the brain of a patient with Parkinson's disease (CT=29.6). Please see Panel 1.3D for a discussion of potential utility in the central nervous system.

Panel CNS_neurodegeneration_v1.0 Summary Expression of the NOV6 gene is ubiquitous throughout the samples in this panel, with highest expression in the hippocampus of a patient with Alzheimer's disease (CT=25.8). While no association between the expression of this gene and the presence of Alzheimer's disease is detected in this panel, these results confirm the expression of this gene in areas that degenerate in Alzheimer's disease, including the cortex, hippocampus, amygdala and thalamus. Synaptotagmin expression is altered in the brain of Alzheimer's patients, possibly explaining impaired synaptogenesis and/or synaptosomal loss secondary to neuronal loss observed in the neurodegenerative disorder. It may also represent, reflect or account for the impaired neuronal transmission in Alzheimer's disease (AD), caused by deterioration of the exocytic machinery. Since the NOV6 gene is a homolog of synaptotagmin, agents that potentiate the expression or function of the protein encoded by the NOV6 gene may be useful in the treatment of Alzheimer's disease. (Reddy et al., Plasma membrane repair is mediated by Ca(2+)-regulated exocytosis of lysosomes. Cell 106:157-69, 2001; Takamori et al., Antibodies to calcium channel and synaptotagmin in Lambert-Eaton myasthenic syndrome. Am J Med Sci. 319:204-8, 2000; Sze et al., Selective regional loss of exocytotic presynaptic vesicle proteins in Alzheimer's disease brains. J Neurol Sci. 175:81-90, 2000; Sokolov et al., Levels of mRNAs encoding synaptic vesicle and synaptic plasma membrane proteins in the temporal cortex of elderly schizophrenic patients. Biol Psychiatry. 48:184-96, 2000; Masliah et al., Altered expression of synaptic proteins occurs early during progression of Alzheimer's disease. Neurology 56:127-9, 2001; Yoo et al., Synaptosomal proteins, beta-soluble N-ethylmaleimide-sensitive factor attachment protein

(beta-SNAP), gamma-SNAP and synaptotagmin I in brain of patients with Down syndrome and Alzheimer's disease. Dement Geriatr Cogn Disord. 12:219-25, 2001).

NOV8: Glypican 2 Precursor-like

- 5 Expression of the NOV8a gene (134913441_EXT) and variants NOV8b (CG50970-02) and NOV8c (CG50970-03) was assessed using the primer-probe sets Ag1309 and Ag2251 described in Tables 41 and 42. Results from RTQ-PCR runs are shown in Tables 43, 44, 45, and 46.

10 Table 41. Probe Name Ag1309

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-ACTCTCTGACCCAGCTCTTCTC-3'	59.3	22	412	126
Probe	TET-5'-CCACTCCTACGGCCGCTGTATG-3'-TAMRA	70.6	23	434	127
Reverse	5'-GAGAACAGGCCATTGAATATGA-3'	59	22	469	128

Table 42. Probe Name Ag2251

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-ACTCTCTGACCCAGCTCTTCTC-3'	59.3	22	359	129
Probe	TET-5'-CCACTCCTACGGCCGCTGTATG-3'-TAMRA	70.6	23	381	130
Reverse	5'-GAGAACAGGCCATTGAATATGA-3'	59	22	416	131

Table 43. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3dtm4197t_ag2251		1.3dtm4197t_ag2251
Liver adenocarcinoma	0.9	Kidney (fetal)	1.9
Pancreas	0.4	Renal ca 786-0	1.0
Pancreatic ca CAPAN 2	0.4	Renal ca. A498	4.5
Adrenal gland	0.6	Renal ca RXF 393	0.0
Thyroid	0.4	Renal ca ACHN	0.3
Salivary gland	1.2	Renal ca UO-31	2.8
Pituitary gland	0.7	Renal ca. TK-10	3.8
Brain (fetal)	73.7	Liver	0.0
Brain (whole)	4.6	Liver (fetal)	1.7
Brain (amygdala)	6.4	Liver ca (hepatoblast) HepG2	1.8
Brain (cerebellum)	1.8	Lung	0.0
Brain (hippocampus)	22.2	Lung (fetal)	3.1
Brain (substantia nigra)	2.1	Lung ca (small cell) LX-1	4.5
Brain (thalamus)	4.5	Lung ca (small cell) NCI-H69	8.7

Cerebral Cortex	3.5	Lung ca. (s.cell var.) SHP-77	25.7
Spinal cord	3.2	Lung ca. (large cell) NCI-H460	2.5
CNS ca. (glio/astro) U87-MG	4.3	Lung ca. (non-sm. cell) A549	2.8
CNS ca. (glio/astro) U-118-MG	2.2	Lung ca. (non-s cell) NCI-H23	12.4
CNS ca. (astro) SW1783	14.3	Lung ca. (non-s.cell) HOP-62	1.7
CNS ca. * (neuro; met) SK-N-AS	100.0	Lung ca. (non-s.cl) NCI-H522	28.1
CNS ca. (astro) SF-539	0.5	Lung ca. (squamous) SW 900	2.1
CNS ca. (astro) SNB-75	13.0	Lung ca. (squamous) NCI-H596	0.7
CNS ca. (glio) SNB-19	14.7	Mammary gland	1.0
CNS ca. (glio) U251	3.6	Breast ca.* (pl. effusion) MCF-7	4.0
CNS ca. (glio) SF-295	3.6	Breast ca.* (pl. ef) MDA-MB-231	1.1
Heart (fetal)	3.4	Breast ca.* (pl. effusion) T47D	1.1
Heart	0.0	Breast ca. BT-549	16.3
Fetal Skeletal	15.2	Breast ca. MDA-N	6.4
Skeletal muscle	0.0	Ovary	3.2
Bone marrow	1.8	Ovarian ca. OVCAR-3	1.7
Thymus	21.2	Ovarian ca. OVCAR-4	0.8
Spleen	0.8	Ovarian ca. OVCAR-5	2.3
Lymph node	1.1	Ovarian ca. OVCAR-8	7.3
Colorectal	0.8	Ovarian ca. IGROV-1	2.4
Stomach	0.6	Ovarian ca.* (ascites) SK-OV-3	0.6
Small intestine	2.6	Uterus	0.8
Colon ca. SW480	2.5	Placenta	0.8
Colon ca.* (SW480 met) SW620	1.5	Prostate	1.1
Colon ca. HT29	1.7	Prostate ca.* (bone met) PC-3	3.2
Colon ca. HCT-116	2.4	Testis	69.7
Colon ca. CaCo-2	2.5	Melanoma Hs688(A) T	0.0
83219 CC Well to Mod Diff (ODO3866)	2.2	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	2.0	Melanoma UACC-62	0.4
Gastric ca.* (liver met) NCI-N87	0.8	Melanoma M14	2.6
Bladder	1.0	Melanoma LOX IMVI	0.7
Trachea	1.8	Melanoma* (met) SK-MEL-5	5.6
Kidney	0.7	Adipose	0.0

Table 44. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2dtm4198t_ag2251		2dtm4198t_ag2251
Normal Colon GENPAK 061003	5.5	Kidney NAT Clontech 8120608	0.0
83219 CC Well to Mod Diff (ODO3866)	4.5	Kidney Cancer Clontech 8120613	0.0
83220 CC NAT (ODO3866)	2.6	Kidney NAT Clontech 8120614	0.6
83221 CC Gr 2 rectosigmoid (ODO3868)	1.2	Kidney Cancer Clontech 9010320	0.0

83222 CC NAT (ODO3868)	1.1	Kidney NAT Clontech 9010321	1.3
83235 CC Mod Diff (ODO3920)	5.8	Normal Uterus GENPAK 061018	1.1
83236 CC NAT (ODO3920)	2.3	Uterus Cancer GENPAK 064011	3.0
83237 CC Gr.2 ascend colon (ODO3921)	4 1	Normal Thyroid Clontech A+ 6570-1	0.6
83238 CC NAT (ODO3921)	0.0	Thyroid Cancer GENPAK 064010	0.6
83241 CC from Partial Hepatectomy (ODO4309)	1 3	Thyroid Cancer INVITROGEN A302152	0.4
83242 Liver NAT (ODO4309)	0.0	Thyroid NAT INVITROGEN A302153	2.3
87472 Colon mets to lung (OD04451-01)	4.3	Normal Breast GENPAK 061019	4.4
87473 Lung NAT (OD04451-02)	0.0	84877 Breast Cancer (OD04566)	1.2
Normal Prostate Clontech A+ 6546-1	0.0	85975 Breast Cancer (OD04590-01)	100.0
84140 Prostate Cancer (OD04410)	3.4	85976 Breast Cancer Mets (OD04590-03)	1.5
84141 Prostate NAT (OD04410)	0 0	87070 Breast Cancer Metastasis (OD04655-05)	3 7
87073 Prostate Cancer (OD04720-01)	0.6	GENPAK Breast Cancer 064006	6 8
87074 Prostate NAT (OD04720-02)	1 8	Breast Cancer Res. Gen. 1024	10.4
Normal Lung GENPAK 061010	5.1	Breast Cancer Clontech 9100266	6 6
83239 Lung Met to Muscle (ODO4286)	0.0	Breast NAT Clontech 9100265	3.4
83240 Muscle NAT (ODO4286)	0.6	Breast Cancer INVITROGEN A209073	7.9
84136 Lung Malignant Cancer (OD03126)	3.9	Breast NAT INVITROGEN A2090734	2.5
84137 Lung NAT (OD03126)	0.0	Normal Liver GENPAK 061009	0.0
84871 Lung Cancer (OD04404)	0.0	Liver Cancer GENPAK 064003	0 6
84872 Lung NAT (OD04404)	0.6	Liver Cancer Research Genetics RNA 1025	0.0
84875 Lung Cancer (OD04565)	0.6	Liver Cancer Research Genetics RNA 1026	0.6
84876 Lung NAT (OD04565)	0.0	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	0 0
85950 Lung Cancer (OD04237-01)	99.3	Paired Liver Tissue Research Genetics RNA 6004-N	0 6
85970 Lung NAT (OD04237-02)	2.4	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	1.1
83255 Ocular Mel Met to Liver (ODO4310)	0.7	Paired Liver Tissue Research Genetics RNA 6005-N	0.0
83256 Liver NAT (ODO4310)	0.0	Normal Bladder GENPAK 061001	1 8
84139 Melanoma Mets to Lung (OD04321)	18.0	Bladder Cancer Research Genetics RNA 1023	2 8
84138 Lung NAT (OD04321)	0.6	Bladder Cancer INVITROGEN A302173	13 2
Normal Kidney GENPAK 061008	1.4	87071 Bladder Cancer (OD04718-01)	0 0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	8.0	87072 Bladder Normal Adjacent (OD04718-03)	1 3
83787 Kidney NAT (OD04338)	0.0	Normal Ovary Res. Gen.	2 8

83788 Kidney Ca Nuclear grade 1/2 (OD04339)	2.4	Ovarian Cancer GENPAK 064008	4.3
83789 Kidney NAT (OD04339)	0.0	87492 Ovary Cancer (OD04768-07)	4.0
83790 Kidney Ca, Clear cell type (OD04340)	1.2	87493 Ovary NAT (OD04768-08)	0.0
83791 Kidney NAT (OD04340)	1.0	Normal Stomach GENPAK 061017	0.8
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.0	Gastric Cancer Clontech 9060358	0.3
83793 Kidney NAT (OD04348)	0.8	NAT Stomach Clontech 9060359	1.2
87474 Kidney Cancer (OD04622-01)	1.1	Gastric Cancer Clontech 9060395	0.0
87475 Kidney NAT (OD04622-03)	0.0	NAT Stomach Clontech 9060394	1.5
85973 Kidney Cancer (OD04450-01)	4.6	Gastric Cancer Clontech 9060397	6.8
85974 Kidney NAT (OD04450-03)	0.6	NAT Stomach Clontech 9060396	0.0
Kidney Cancer Clontech 8120607	0.6	Gastric Cancer GENPAK 064005	2.5

Table 45. Panel 4D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	4dtm4199t_ag2251	4Dtm1886t_ag1309
93768_Secondary Th1_anti-CD28/anti-CD3	1.6	1.5
93769_Secondary Th2_anti-CD28/anti-CD3	1.2	1.0
93770_Secondary Tr1_anti-CD28/anti-CD3	1.7	2.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.5	1.7
93572_Secondary Th2_resting day 4-6 in IL-2	0.6	1.4
93571_Secondary Tr1_resting day 4-6 in IL-2	1.2	1.4
93568_primary Th1_anti-CD28/anti-CD3	2.7	1.7
93569_primary Th2_anti-CD28/anti-CD3	1.9	3.4
93570_primary Tr1_anti-CD28/anti-CD3	1.2	5.9
93565_primary Th1_resting dy 4-6 in IL-2	17.1	12.5
93566_primary Th2_resting dy 4-6 in IL-2	8.6	6.5
93567_primary Tr1_resting dy 4-6 in IL-2	2.4	3.7
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	1.2	3.2
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	2.7	4.3
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	1.9	1.1
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.9	1.7
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	1.0	1.1
93354_CD4_none	0.5	1.4
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	1.7	4.5
93103_LAK cells_resting	1.6	1.2
93788_LAK cells_IL-2	1.8	3.1
93787_LAK cells_IL-2+IL-12	0.7	1.8
93789_LAK cells_IL-2+IFN gamma	1.3	1.7
93790_LAK cells_IL-2+ IL-18	1.4	1.5

93104_LAK cells_PMA/ionomycin and IL-18	0.0	0.8
93578_NK Cells IL-2_resting	1.1	0.9
93109_Mixed Lymphocyte Reaction_Two Way MLR	2.3	1.6
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.3	1.7
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.4	0.8
93112_Mononuclear Cells (PBMCs)_resting	0.0	0.4
93113_Mononuclear Cells (PBMCs)_PWM	2.1	6.1
93114_Mononuclear Cells (PBMCs)_PHA-L	5.7	9.9
93249_Ramos (B cell)_none	6.2	13.6
93250_Ramos (B cell)_ionomycin	24.3	34.9
93349_B lymphocytes_PWM	7.3	7.4
93350_B lymphocytes_CD40L and IL-4	4.4	2.7
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	2.3	2.6
93248_EOL-1 (Eosinophil)_dbcAMP/PMA/ionomycin	1.3	0.3
93356_Dendritic Cells_none	0.8	0.5
93355_Dendritic Cells_LPS 100 ng/ml	0.0	0.0
93775_Dendritic Cells_anti-CD40	0.0	0.3
93774_Monocytes_resting	0.0	0.3
93776_Monocytes_LPS 50 ng/ml	0.3	1.1
93581_Macrophages_resting	1.3	0.6
93582_Macrophages_LPS 100 ng/ml	0.0	0.0
93098_HUVEC (Endothelial)_none	3.5	5.3
93099_HUVEC (Endothelial)_starved	12.4	12.7
93100_HUVEC (Endothelial)_IL-1b	1.6	1.3
93779_HUVEC (Endothelial)_IFN gamma	2.5	2.9
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.1	1.5
93101_HUVEC (Endothelial)_TNF alpha + IL4	2.6	3.5
93781_HUVEC (Endothelial)_IL-11	1.4	4.4
93583_Lung Microvascular Endothelial Cells_none	2.3	1.3
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.7	2.1
92662_Microvascular Dermal endothelium_none	2.6	6.1
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.3	2.0
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	1.6	2.9
93347_Small Airway Epithelium_none	0.4	0.8
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.5	3.1
92668_Coronary Artery SMC_resting	1.1	1.3
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	2.0	1.4
93107_astrocytes_resting	22.5	17.8
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	4.7	6.2
92666_KU-812 (Basophil)_resting	0.2	0.3
92667_KU-812 (Basophil)_PMA/ionomycin	0.3	1.2
93579_CCD1106 (Keratinocytes)_none	3.9	3.9
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	3.1	19.5

93791_Liver Cirrhosis	2.6	2.0
93792_Lupus Kidney	0.0	0.3
93577_NCI-H292	0.4	0.7
93358_NCI-H292_IL-4	0.4	1.7
93360_NCI-H292_IL-9	1.6	0.0
93359_NCI-H292_IL-13	1.6	0.6
93357_NCI-H292_IFN gamma	0.3	0.0
93777_HPAEC_-	2.0	3.3
93778_HPAEC_IL-1 beta/TNA alpha	0.6	1.6
93254_Normal Human Lung Fibroblast_none	3.4	3.7
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	1.5	1.6
93257_Normal Human Lung Fibroblast_IL-4	2.8	3.6
93256_Normal Human Lung Fibroblast_IL-9	3.2	2.6
93255_Normal Human Lung Fibroblast_IL-13	2.8	2.7
93258_Normal Human Lung Fibroblast_IFN gamma	1.9	0.5
93106_Dermal Fibroblasts CCD1070_resting	3.7	4.2
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	4.2	2.4
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	2.5	1.3
93772_dermal fibroblast_IFN gamma	0.2	0.7
93771_dermal fibroblast_IL-4	0.8	0.7
93260_IBD Colitis 2	0.0	0.2
93261_IBD Crohns	0.0	0.0
735010_Colon_normal	4.2	3.1
735019_Lung_none	1.3	1.5
64028-1_Thymus_none	0.3	1.6
64030-1_Kidney_none	100.0	100.0

Table 46. Panel CNS_neurodegeneration_v1.0

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm6901t_ag2251_a2s2		tm6901t_ag2251_a2s2
106655_4951 Hippo	19.7	106677_4624 BA21	3.4
106657_4986 Hippo	35.8	106681_4640 BA21	34.1
106652_4933 Hippo	7.2	106654_4951 BA17	19.5
106649_4901 Hippo	9.7	cns_water	0.0
110138_3087 hippo	59.0	106651_4933 BA17	17.3
110121_3027 Hippo	97.7	106648_4901 BA17	19.1
106670_4971 Hippo	37.0	110123_3027 Occ Ctx	52.8
106666_4867 Hippo	34.8	110140_3087 occ ctx	41.9
106680_4624 Hippo	17.2	106659_4595 BA17	6.3
106653_4951 BA21	20.5	106668_4971 BA17	51.5
106656_4986 BA21	33.7	106662_4737 BA17	22.9
106650_4933 BA21	9.8	106665_4867 BA17	6.6

106647_4901 BA21	36.0	106675_3975 BA17	73.6
110136_3087 inf temp ctx	76.8	106672_3954 BA17	16.7
110137_3087 sup temp ctx	97.7	106678_4624 BA17	11.8
110118_3027 Inf Temp Ctx	59.8	106682_4640 BA17	28.1
110119_3027 Sup Temp Ctx	100.0	106660_4595 BA7	12.0
106658_4595 BA21	9.8	113670_106669 pool	62.2
106667_4971 BA21	29.9	106663_4737 BA7	20.3
106661_4737 BA21	10.5	106676_3975 BA7	43.7
106664_4867 BA21	34.1	106673_3954 BA7	14.9
106674_3975 BA21	63.8	106679_4624 BA7	7.8
106671_3954 BA21	13.7	106683_4640 BA7	29.8

Panel 1.3D Summary Ag2251 The highest level of expression of the NOV8 gene is seen in a CNS cancer cell line SK-N-AS (CT=29.6). The gene is also expressed at higher levels in cell lines derived from lung, prostate, and breast cancers compared to the normal tissues and may play a role in these cancers. Thus, expression of the NOV8 gene could be used as a marker or as a therapeutic for lung, prostate and breast cancer. In addition, therapeutic modulation of the activity of the product of this gene, through the use of peptides, antibodies, chimeric molecules or small molecule drugs, may be useful in the treatment of these cancers.

The NOV8 gene is also expressed at higher levels in fetal liver, lung, skeletal muscle, and heart (CTs=32-35) when compared to the expression in adult tissues (CTs=40). These results suggest that expression of the NOV8 gene could potentially be used to distinguish between the adult and fetal phenotypes of these tissues. Furthermore, the difference in expression in fetal and adult tissue may also indicate an involvement of the gene product in the differentiation processes leading to the formation of the adult organs. Therefore, the protein encoded by the NOV8 gene could potentially play a role in the regeneration of these tissues in the adult.

The NOV8 gene, a glypican homolog, is expressed at moderate to low levels across many regions of the brain. These regions include the hippocampus, amygdala, thalamus and cerebral cortex, all of which are key regions subject to Alzheimer's disease neurodegeneration. Furthermore, glypican is expressed in senile plaques and neurofibrillary tangles, also indicating a role in Alzheimer's disease. Therefore, the expression profile of the NOV8 gene suggests that antibodies against the protein encoded by the NOV8 gene can be used to distinguish neurodegenerative disease in the human brain. Furthermore, since NOV8 gene-product-like substances are components of senile plaques which are thought to give rise to the dementia pathology of Alzheimer's disease, agents that target this gene and disrupt its role in

senile plaques may have utility in treating the cause and symptoms of Alzheimer's disease as well as other neurodegenerative diseases that involve this glypican.

Panel 2D Summary Ag2251 The highest expression of NOV8 gene is seen in a breast cancer sample (CT = 30.3). The expression of this gene appears to show an association with samples derived from colon, lung, kidney, breast, bladder and gastric cancers when compared to the matched normal tissue. Thus, expression of the NOV8 gene could be used as a marker for these cancers. In addition, therapeutic activity of the product of this gene, through the use of peptides, antibodies, chimeric molecules or small molecule drugs, may be useful in the treatment of colon, lung, kidney, breast, bladder and gastric cancers.

Panel 4D Summary Ag2251/Ag1309 Two experiments using two different probe and primer sets produce results that are in very good agreement, with highest expression seen in the kidney (CTs=28-29). This high level of expression in the kidney suggests that expression of the NOV8 gene can serve as a marker for kidney tissue. The NOV8 gene is also expressed at low level in activated Ramos B cell line, in activated primary B cells, Th1 T cells, activated HUVEC and keratinocytes. The NOV8 gene encodes for a protein that is a homolog of a glypican molecule, which belongs to the family of HSPG (heparan sulfate proteoglycans). Glypicans can regulate the activity of a wide variety of growth and survival factors. Therefore, therapeutic modulation of the expression or function of this gene or gene product, through the use of antibody drugs could potentially prevent T and B cell activation in the treatment of autoimmune mediated diseases such as insulin-dependent diabetes mellitus, rheumatoid arthritis, Crohn's disease, allergies, delayed type hypersensitivity, asthma, and psoriasis.

Panel CNS_neurodegeneration_v1.0 Summary Ag2251 Highest expression of the NOV8 gene in this panel is detected in the cerebral cortex of an Alzheimer's patient (CT=32.7). While no association between the expression of this gene and the presence of Alzheimer's disease is detected in this panel, these results confirm the expression of this gene in areas that degenerate in Alzheimer's disease. Please see Panel 1.3D for a discussion of potential utility of this gene in the central nervous system. (Verbeek et al., Agrin is a major heparan sulfate proteoglycan accumulating in Alzheimer's disease brain. Am J Pathol. 155:2115-25, 1999).

NOV9: Mitogen-Activated-Protein Kinase Kinase 2-like

Expression of NOV9 gene (also referred to as AC011005_da2) was assessed using the primer-probe set Ag2022 described in Tables 47. Results from RTQ-PCR runs are shown in Tables 48, 49, and 50.

Table 47. Probe Name Ag2022

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CCAGGAGTTTGTCAATAAATGC-3'	58.6	22	800	132
Probe	FAM-5'-CTCATCAAGAACCCAGCGGAGCG-3'-TAMRA	71.2	23	822	133
Reverse	5'-TTGATGAAGGTGTGGTTTGTG-3'	59.5	21	863	134

Table 48. Panel 1.3D

Tissue Name	Relative Expression(%)	
	1.3dx4tm5437 f_ag2022 b1	1.3dx4tm5441 f_ag2022 a1
Liver adenocarcinoma	23.1	15.9
Pancreas	9.6	4.3
Pancreatic ca. CAPAN 2	4.1	4.4
Adrenal gland	7.9	10.3
Thyroid	12.1	9.7
Salivary gland	10.9	5.9
Pituitary gland	12.0	9.6
Brain (fetal)	13.6	7.6
Brain (whole)	47.3	25.1
Brain (amygdala)	33.7	19.9
Brain (cerebellum)	33.2	16.3
Brain (hippocampus)	42.8	21.7
Brain (substantia nigra)	30.6	13.8
Brain (thalamus)	50.3	24.6
Cerebral Cortex	36.5	31.4
Spinal cord	16.9	8.7
CNS ca. (glio/astro) U87-MG	17.6	18.5
CNS ca. (glio/astro) U-118-MG	54.6	38.5
CNS ca. (astro) SW1783	13.5	12.8
CNS ca.* (neuro; met) SK-N-AS	15.4	12.9
CNS ca. (astro) SF-539	14.3	9.5
CNS ca. (astro) SNB-75	29.6	25.8
CNS ca. (glio) SNB-19	23.7	17.9
CNS ca. (glio) U251	38.4	34.5
CNS ca. (glio) SF-295	18.5	17.2
Heart (fetal)	17.1	16.3
Heart	25.8	10.3
Fetal Skeletal	12.2	12.9
Skeletal muscle	100.0	100.0
Bone marrow	15.0	14.5
Thymus	7.6	8.1
Spleen	14.5	11.4
Lymph node	25.7	19.2

Colorectal	6.7	4.7
Stomach	14.4	10.1
Small intestine	30.2	32.3
Colon ca. SW480	9.2	6.7
Colon ca. * (SW480 met)SW620	3.1	4.1
Colon ca. HT29	1.4	2.6
Colon ca. HCT-116	8.5	9.1
Colon ca. CaCo-2	5.6	7.1
83219 CC Well to Mod Diff (ODO3866)	11.8	11.5
Colon ca. HCC-2998	4.6	7.2
Gastric ca. * (liver met) NCI-N87	13.1	9.3
Bladder	3.4	4.2
Trachea	13.7	10.5
Kidney	14.6	6.4
Kidney (fetal)	9.2	4.2
Renal ca. 786-0	9.5	7.3
Renal ca. A498	23.2	19.4
Renal ca. RXF 393	16.9	16.0
Renal ca. ACHN	14.4	10.5
Renal ca. UO-31	11.2	8.1
Renal ca. TK-10	5.4	4.8
Liver	11.2	3.4
Liver (fetal)	24.1	18.8
Liver ca. (hepatoblast) HepG2	12.8	10.0
Lung	11.4	11.9
Lung (fetal)	11.8	8.9
Lung ca. (small cell) LX-1	12.4	8.4
Lung ca. (small cell) NCI-H69	15.8	17.0
Lung ca. (s.cell var.) SHP-77	11.2	12.7
Lung ca. (large cell)NCI-H460	30.6	28.4
Lung ca. (non-sm. cell) A549	5.7	6.2
Lung ca. (non-s.cell) NCI-H23	6.3	7.0
Lung ca. (non-s.cell) HOP-62	13.1	12.0
Lung ca. (non-s.cl) NCI-H522	5.7	4.6
Lung ca. (squam.) SW 900	3.6	4.1
Lung ca. (squam.) NCI-H596	12.2	11.1
Mammary gland	7.2	8.9
Breast ca. * (pl. effusion) MCF-7	9.6	9.1
Breast ca. * (pl.ef) MDA-MB-231	46.9	56.9
Breast ca. * (pl effusion) T47D	4.7	4.6
Breast ca. BT-549	19.6	20.7
Breast ca. MDA-N	6.3	6.2
Ovary	7.3	6.5
Ovarian ca. OVCAR-3	7.4	5.6

Ovarian ca. OVCAR-4	28.0	20.7
Ovarian ca. OVCAR-5	7.0	7.0
Ovarian ca. OVCAR-8	11.7	9.8
Ovarian ca. IGROV-1	3.5	2.3
Ovarian ca * (ascites) SK-OV-3	23.7	17.0
Uterus	25.9	18.7
Placenta	10.9	6.3
Prostate	10.5	10.5
Prostate ca. * (bone met) PC-3	20.5	18.1
Testis	27.2	19.5
Melanoma Hs688(A).T	6.6	5.1
Melanoma* (met) Hs688(B).T	10.7	8.5
Melanoma UACC-62	43.5	36.3
Melanoma M14	42.1	37.0
Melanoma LOX IMVI	7.9	9.1
Melanoma* (met) SK-MEL-5	16.0	14.2
Adipose	4.8	3.8

Table 49. Panel 2.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2.2x4tm6395f ag2022_b1		2.2x4tm6395f ag2022_b1
Normal Colon GENPAK 061003	24.5	83793 Kidney NAT (OD04348)	70.6
97759 Colon cancer (OD06064)	14.3	98938 Kidney malignant cancer (OD06204B)	22.0
97760 Colon cancer NAT (OD06064)	18.0	98939 Kidney normal adjacent tissue (OD06204E)	18.7
97778 Colon cancer (OD06159)	12.2	85973 Kidney Cancer (OD04450-01)	48.2
97779 Colon cancer NAT (OD06159)	18.1	85974 Kidney NAT (OD04450-03)	16.6
98861 Colon cancer (OD06297-04)	15.5	Kidney Cancer Clontech 8120613	14.1
98862 Colon cancer NAT (OD06297-015)	23.7	Kidney NAT Clontech 8120614	40.5
83237 CC Gr.2 ascend colon (ODO3921)	25.7	Kidney Cancer Clontech 9010320	20.5
83238 CC NAT (ODO3921)	21.9	Kidney NAT Clontech 9010321	12.9
97766 Colon cancer metastasis (OD06104)	6.0	Kidney Cancer Clontech 8120607	48.0
97767 Lung NAT (OD06104)	19.5	Kidney NAT Clontech 8120608	37.8
87472 Colon mets to lung (OD04451-01)	30.2	Normal Uterus GENPAK 061018	11.9
87473 Lung NAT (OD04451-02)	11.4	Uterus Cancer GENPAK 064011	16.7
Normal Prostate Clontech A+ 6546-1 (8090438)	21.9	Normal Thyroid Clontech A+ 6570-1 (7080817)	9.6
84140 Prostate Cancer (OD04410)	9.1	Thyroid Cancer GENPAK 064010	19.0
84141 Prostate NAT (OD04410)	11.2	Thyroid Cancer INVITROGEN A302152	28.3

Normal Ovary Res. Gen.	58.3	Thyroid NAT INVITROGEN A302153	11.8
98863 Ovarian cancer (OD06283-03)	12.9	Normal Breast GENPAK 061019	12.3
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	8.5	84877 Breast Cancer (OD04566)	12.9
Ovarian Cancer GENPAK 064008	15.8	Breast Cancer Res Gen. 1024	23.1
97773 Ovarian cancer (OD06145)	19.1	85975 Breast Cancer (OD04590-01)	45.8
97775 Ovarian cancer NAT (OD06145)	34.4	85976 Breast Cancer Mets (OD04590-03)	35.7
98853 Ovarian cancer (OD06455-03)	11.0	87070 Breast Cancer Metastasis (OD04655-05)	100.0
98854 Ovarian NAT (OD06455-07) Fallopian tube	2.8	GENPAK Breast Cancer 064006	19.3
Normal Lung GENPAK 061010	11.2	Breast Cancer Clontech 9100266	8.3
92337 Invasive poor diff lung adeno (ODO4945-01)	19 1	Breast NAT Clontech 9100265	9.3
92338 Lung NAT (ODO4945-03)	9 9	Breast Cancer INVITROGEN A209073	3.6
84136 Lung Malignant Cancer (OD03126)	22.4	Breast NAT INVITROGEN A2090734	22.0
84137 Lung NAT (OD03126)	8.6	97763 Breast cancer (OD06083)	47.4
90372 Lung Cancer (OD05014A)	24.5	97764 Breast cancer node metastasis (OD06083)	48.8
90373 Lung NAT (OD05014B)	13.8	Normal Liver GENPAK 061009	29.2
97761 Lung cancer (OD06081)	12.4	Liver Cancer Research Genetics RNA 1026	31.1
97762 Lung cancer NAT (OD06081)	2.6	Liver Cancer Research Genetics RNA 1025	39.1
85950 Lung Cancer (OD04237-01)	14 4	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	35.9
85970 Lung NAT (OD04237-02)	29.6	Paired Liver Tissue Research Genetics RNA 6004-N	8.1
83255 Ocular Mel Met to Liver (ODO4310)	44.3	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	74 1
83256 Liver NAT (ODO4310)	12.2	Paired Liver Tissue Research Genetics RNA 6005-N	74.3
84139 Melanoma Mets to Lung (OD04321)	32.4	Liver Cancer GENPAK 064003	45.7
84138 Lung NAT (OD04321)	13.2	Normal Bladder GENPAK 061001	19.3
Normal Kidney GENPAK 061008	14.8	Bladder Cancer Research Genetics RNA 1023	29.9
83786 Kidney Ca, Nuclear grade 2 (OD04338)	40.8	Bladder Cancer INVITROGEN A302173	30.8
83787 Kidney NAT (OD04338)	12 3	Normal Stomach GENPAK 061017	48.5
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	49.2	Gastric Cancer Clontech 9060397	16.4
83789 Kidney NAT (OD04339)	17.9	NAT Stomach Clontech 9060396	33.1
83790 Kidney Ca, Clear cell type (OD04340)	21 0	Gastric Cancer Clontech 9060395	14.5
83791 Kidney NAT (OD04340)	18 0	NAT Stomach Clontech 9060394	34.4
83792 Kidney Ca, Nuclear grade 3 (OD04348)	16 6	Gastric Cancer GENPAK 064005	25.3

Table 50. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4dx4tm4449f_ag2022_b1		4dx4tm4449f_ag2022_b1
93768_Secondary Th1_anti-CD28/anti-CD3	21.3	93100_HUVEC (Endothelial)_IL-1b	3.8
93769_Secondary Th2_anti-CD28/anti-CD3	16.3	93779_HUVEC (Endothelial)_IFN gamma	15.3
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	13.4
93573_Secondary Th1_resting day 4-6 in IL-2	5.2	93101_HUVEC (Endothelial)_TNF alpha + IL4	13.7
93572_Secondary Th2_resting day 4-6 in IL-2	6.7	93781_HUVEC (Endothelial)_IL-11	13.7
93571_Secondary Tr1_resting day 4-6 in IL-2	6.3	93583_Lung Microvascular Endothelial Cells_none	14.8
93568_primary Th1_anti-CD28/anti-CD3	15.6	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	18.0
93569_primary Th2_anti-CD28/anti-CD3	12.9	92662_Microvascular Dermal endothelium_none	22.2
93570_primary Tr1_anti-CD28/anti-CD3	20.1	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	18.8
93565_primary Th1_resting dy 4-6 in IL-2	23.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	5.8
93566_primary Th2_resting dy 4-6 in IL-2	11.4	93347_Small Airway Epithelium_none	6.9
93567_primary Tr1_resting dy 4-6 in IL-2	1.6	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	25.1
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	12.7	92668_Coronary Artery SMC_resting	18.5
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	11.4	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	14.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	12.4	93107_astrocytes_resting	12.6
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	11.9	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	15.4
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	11.4	92666_KU-812 (Basophil)_resting	58.7
93354_CD4_none	3.2	92667_KU-812 (Basophil)_PMA/ionoycin	100.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	9.0	93579_CCD1106 (Keratinocytes)_none	14.2
93103_LAK cells_resting	10.6	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	1.7
93788_LAK cells_IL-2	12.8	93791_Liver Cirrhosis	1.6
93787_LAK cells_IL-2+IL-12	9.3	93792_Lupus Kidney	1.4
93789_LAK cells_IL-2+IFN	11.3	93577_NCI-H292	19.8

gamma			
93790_LAK cells_IL-2+ IL-18	9.3	93358_NCI-H292_IL-4	20.4
93104_LAK cells_PMA/ionomycin and IL-18	5.7	93360_NCI-H292_IL-9	22.3
93578_NK Cells_IL-2_resting	9.7	93359_NCI-H292_IL-13	12.5
93109_Mixed Lymphocyte Reaction_Two Way MLR	9.2	93357_NCI-H292_IFN gamma	12.9
93110_Mixed Lymphocyte Reaction_Two Way MLR	11.5	93777_HPAEC_-	16.3
93111_Mixed Lymphocyte Reaction_Two Way MLR	7.5	93778_HPAEC_IL-1 beta/TNA alpha	17.5
93112_Mononuclear Cells (PBMcs)_resting	3.9	93254_Normal Human Lung Fibroblast_none	23.0
93113_Mononuclear Cells (PBMcs)_PWM	24.7	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	14.3
93114_Mononuclear Cells (PBMcs)_PHA-L	12.6	93257_Normal Human Lung Fibroblast_IL-4	30.8
93249_Ramos (B cell)_none	13.6	93256_Normal Human Lung Fibroblast_IL-9	27.0
93250_Ramos (B cell)_ionomycin	32.2	93255_Normal Human Lung Fibroblast_IL-13	19.5
93349_B lymphocytes_PWM	49.8	93258_Normal Human Lung Fibroblast_IFN gamma	27.4
93350_B lymphocytes_CD40L and IL-4	25.5	93106_Dermal Fibroblasts CCD1070_resting	24.5
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	18.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	47.3
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	27.5	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	21.4
93356_Dendritic Cells_none	10.0	93772_dermal fibroblast_IFN gamma	12.4
93355_Dendritic Cells_LPS 100 ng/ml	6.9	93771_dermal fibroblast_IL-4	22.5
93775_Dendritic Cells_anti-CD40	8.9	93260_IBD Colitis 2	0.8
93774_Monocytes_resting	11.1	93261_IBD Crohns	1.3
93776_Monocytes_LPS 50 ng/ml	7.0	735010_Colon_normal	13.7
93581_Macrophages_resting	12.4	735019_Lung_none	8.6
93582_Macrophages_LPS 100 ng/ml	5.8	64028-1_Thymus_none	9.9
93098_HUVEC (Endothelial)_none	22.1	64030-1_Kidney_none	18.6
93099_HUVEC (Endothelial)_starved	22.3		

Panel 1.3D Summary Two results using the same probe and primer set show results that are in excellent agreement, with highest expression of the NOV9 gene in adult skeletal muscle (CTs=27). The NOV9 gene also shows moderate expression in other tissues with metabolic function including adipose, adult and fetal heart and liver, adult skeletal muscle, pancreas, and the adrenal, thyroid, and pituitary glands. Expression is much lower in fetal

skeletal muscle (CTs=30) relative to the adult tissue (CTs=27), which may implicate the expression of this gene in differentiation of skeletal muscle and thus suggests that expression of the NOV9 gene could be used to differentiate between the adult and fetal phenotypes of this tissue. The pathway mediated by MAP kinase kinase (MAPKK) has been shown to influence myoblast proliferation and both insulin and exercise stimulate signaling via this pathway in skeletal muscle. Insulin resistance in obese and diabetic subjects may in part be due to tumor necrosis factor alpha, whose effects are mediated through interference with the normal activation of MAPKK by insulin. In addition, exercise training significantly improves insulin-induced MAPKK activity in obese Zucker rats. This indicates that an activator of this kinase may be an effective pharmaceutical agent in the treatment of diabetes. Furthermore, activation of the MAPKK pathway is involved in adipocyte differentiation from preadipocytes in androgen deficiency. Therefore, a MAPKK antagonist may be a suitable pharmacological agent in the treatment of obesity in some cases.

The NOV9 gene is expressed at higher levels in cell lines derived from melanoma, and kidney and lung cancers compared to the normal tissues and may play a role in cancers in these tissues. Thus, the expression of this gene could be useful as a marker or as a therapeutic for lung and kidney cancer as well as melanomas. In addition, therapeutic modulation of the activity of the gene product, through the use of peptides, chimeric molecules or small molecule drugs, may be useful in the therapy of these cancers.

The NOV9 gene, a homolog of Mitogen Activated Protein Kinase Kinase, is expressed at high to moderate levels across the brain, with highest expression in the central nervous seen in the thalamus (CT=28.4). Mitogen Activated Protein Kinase Kinase is activated by Valproic acid, a drug that is used to treat both seizure disorders and bipolar depression. Valproic acid is believed to work by increasing neuronal production of GABA, the major inhibitory neurotransmitter in the brain. Selective activation of this kinase may therefore have therapeutic benefit in the treatment of seizure disorders, bipolar disorder, or in any other neurological/psychiatric condition believed to be caused by a GABA deficit (schizophrenia).

Panel 2.2 Summary Highest expression of the NOV9 gene in this panel is seen in a breast cancer sample (CT = 29.0). The expression of this gene shows an association with samples derived from breast and kidney cancers when compared to the matched normal tissue. Thus, expression of the NOV9 gene could be useful as a marker for breast and kidney cancers. Furthermore, therapeutic activity of the product of this gene, through the use of peptides, chimeric molecules or small molecule drugs, may be useful in the treatment of breast and kidney cancers.

Panel 4D Summary Expression of the NOV9 gene is ubiquitous throughout this panel.

Highest expression of this gene is found in the basophil cell line, KU-812, upon activation with PMA/ionomycin (CT=26.2), compared to non-activated cells. High expression of the NOV9 gene is also found on activated B cells, a B cell line, and dermal fibroblasts. The NOV9 gene is homologous to a Mitogen Activated Protein Kinase Kinase 2 (MAPKK2), a serine threonine kinase which functions downstream of Raf in the signaling pathway that affects proliferation and differentiation. The high expression of this kinase on basophiles suggests a role for this kinase in mast cell/basophile signal transduction. Activated mast/basophile cells have been associated with many atopic diseases, including asthma, atopic contact dermatitis, allergies, and rhinitis. Therefore, therapeutic modulation of the expression or function of the NOV9 gene product, through the use of small molecule drugs, might be beneficial in the treatment of these diseases. In addition, the high expression of this kinase in activated B cells suggests that the use of small molecule drugs designed to the NOV9 gene product could prevent B cell hyperproliferative disorders such as autoimmune diseases and lymphomas (Yuan et al., The mood stabilizer valproic acid activates mitogen-activated protein kinases and promotes neurite growth. *J Biol Chem.* 276:31674-83, 2001; Bulleit and Hsieh, MEK inhibitors block BDNF-dependent and -independent expression of GABA(A) receptor subunit mRNAs in cultured mouse cerebellar granule neurons. *Brain Res Dev Brain Res.* 119:1-10, 2000; Jones et al., ERK1/2 is required for myoblast proliferation but is dispensable for muscle gene expression and cell fusion. *J Cell Physiol.* 186:104-15, 2001; Wojtaszewski et al., Differential regulation of MAP kinase by contraction and insulin in skeletal muscle: metabolic implications. *Am J Physiol.* 277(4 Pt 1):E724-32, 1999; Begum et al., Effect of tumor necrosis factor-alpha on insulin-stimulated mitogen-activated protein kinase cascade in cultured rat skeletal muscle cells. *Eur J. Biochem.* 238:214-20, 1996; Osman et al., Exercise training increases ERK2 activity in skeletal muscle of obese Zucker rats. *J Appl Physiol.* 90:454-60, 2001; Lacasa et al., Site-related specificities of the control by androgenic status of adipogenesis and mitogen-activated protein kinase cascade/c-fos signaling pathways in rat preadipocytes. *Endocrinology* 138:3181-6, 1997).

NOV11: Thymosin beta 10-like

Expression of the NOV11a gene (GMAC079400_A) and variant NOV11b (CG109754-01) was assessed using the primer-probe sets Ag2431 and Ag3087 described in Tables 51. Results from RTQ-PCR runs are shown in Tables 52, 53, 54, and 55.

Table 51. Probe Name Ag2431

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-AGAAAATGGCAGACAAACCA-3'	58.2	20	23	135
Probe	TET-5'-AATCGCCAGCTTCAATAGGGCCAAG-3'-TAMRA	70.7	25	54	136
Reverse	5'-GCGTCTCCGTTTCTTCAG-3'	58.6	19	79	137

Table 52. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3dtm4242t_ag2431		1.3dtm4242t_ag2431
Liver adenocarcinoma	13.7	Kidney (fetal)	3.6
Pancreas	0.9	Renal ca. 786-0	2.4
Pancreatic ca. CAPAN 2	0.4	Renal ca. A498	3.6
Adrenal gland	3.0	Renal ca. RXF 393	0.5
Thyroid	0.9	Renal ca. ACHN	0.1
Salivary gland	1.2	Renal ca. UO-31	0.2
Pituitary gland	1.5	Renal ca. TK-10	0.3
Brain (fetal)	28.1	Liver	1.6
Brain (whole)	2.2	Liver (fetal)	3.6
Brain (amygdala)	24.1	Liver ca. (hepatoblast) HepG2	0.8
Brain (cerebellum)	1.5	Lung	8.6
Brain (hippocampus)	100.0	Lung (fetal)	5.0
Brain (substantia nigra)	1.9	Lung ca. (small cell) LX-1	1.4
Brain (thalamus)	6.3	Lung ca. (small cell) NCI-H69	1.1
Cerebral Cortex	20.6	Lung ca. (s.cell var.) SHP-77	1.4
Spinal cord	1.0	Lung ca. (large cell) NCI-H460	1.0
CNS ca. (glio/astro) U87-MG	9.4	Lung ca. (non-sm. cell) A549	1.7
CNS ca. (glio/astro) U-118-MG	6.5	Lung ca. (non-s.cell) NCI-H23	1.4
CNS ca. (astro) SW1783	3.5	Lung ca. (non-s.cell) HOP-62	0.4
CNS ca. * (neuro; met) SK-N-AS	5.6	Lung ca. (non-s.cl) NCI-H522	0.8
CNS ca. (astro) SF-539	1.5	Lung ca. (squamous) SW 900	1.6
CNS ca. (astro) SNB-75	3.9	Lung ca. (squamous) NCI-H596	0.5
CNS ca. (glio) SNB-19	1.8	Mammary gland	3.3
CNS ca. (glio) U251	0.6	Breast ca.* (pl. effusion) MCF-7	3.8
CNS ca. (glio) SF-295	0.4	Breast ca.* (pl.ef) MDA-MB-231	32.3
Heart (fetal)	3.1	Breast ca.* (pl. effusion) T47D	0.2
Heart	1.5	Breast ca. BT-549	25.3
Fetal Skeletal	6.8	Breast ca. MDA-N	1.0
Skeletal muscle	0.5	Ovary	4.5
Bone marrow	7.9	Ovarian ca. OVCAR-3	1.1
Thymus	0.6	Ovarian ca. OVCAR-4	0.1
Spleen	2.5	Ovarian ca. OVCAR-5	0.6
Lymph node	4.4	Ovarian ca. OVCAR-8	1.1

Colorectal	3.8	Ovarian ca. IGROV-1	0.8
Stomach	1.4	Ovarian ca.* (ascites) SK-OV-3	2.9
Small intestine	3.2	Uterus	1.5
Colon ca. SW480	1.1	Placenta	1.7
Colon ca.* (SW480 met)SW620	0.7	Prostate	1.4
Colon ca. HT29	1.7	Prostate ca.* (bone met)PC-3	1.5
Colon ca. HCT-116	1.6	Testis	0.7
Colon ca. CaCo-2	0.8	Melanoma Hs688(A).T	3.4
83219 CC Well to Mod Diff (ODO3866)	5.3	Melanoma* (met) Hs688(B).T	1.6
Colon ca. HCC-2998	3.8	Melanoma UACC-62	0.5
Gastric ca.* (liver met) NCI-N87	4.7	Melanoma M14	1.2
Bladder	8.4	Melanoma LOX IMVI	12.7
Trachea	3.1	Melanoma* (met) SK-MEL-5	2.8
Kidney	1.2	Adipose	3.7

Table 53. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2dtm4243t_ag2431		2dtm4243t_ag2431
Normal Colon GENPAK 061003	33.0	Kidney NAT Clontech 8120608	1.1
83219 CC Well to Mod Diff (ODO3866)	21.8	Kidney Cancer Clontech 8120613	1.4
83220 CC NAT (ODO3866)	19.8	Kidney NAT Clontech 8120614	1.3
83221 CC Gr.2 rectosigmoid (ODO3868)	26.6	Kidney Cancer Clontech 9010320	5.0
83222 CC NAT (ODO3868)	2.1	Kidney NAT Clontech 9010321	3.0
83235 CC Mod Diff (ODO3920)	26.1	Normal Uterus GENPAK 061018	1.6
83236 CC NAT (ODO3920)	13.9	Uterus Cancer GENPAK 064011	7.1
83237 CC Gr.2 ascend colon (ODO3921)	49.7	Normal Thyroid Clontech A+ 6570-1	1.4
83238 CC NAT (ODO3921)	8.4	Thyroid Cancer GENPAK 064010	5.2
83241 CC from Partial Hepatectomy (ODO4309)	13.9	Thyroid Cancer INVITROGEN A302152	2.7
83242 Liver NAT (ODO4309)	3.9	Thyroid NAT INVITROGEN A302153	2.8
87472 Colon mets to lung (OD04451-01)	5.6	Normal Breast GENPAK 061019	3.2
87473 Lung NAT (OD04451-02)	6.7	84877 Breast Cancer (OD04566)	1.9
Normal Prostate Clontech A+ 6546-1	1.4	85975 Breast Cancer (OD04590-01)	3.4
84140 Prostate Cancer (OD04410)	7.4	85976 Breast Cancer Mets (OD04590-03)	4.7
84141 Prostate NAT (OD04410)	6.4	87070 Breast Cancer Metastasis (OD04655-05)	8.0
87073 Prostate Cancer (OD04720-01)	3.2	GENPAK Breast Cancer 064006	7.9
87074 Prostate NAT (OD04720-02)	6.2	Breast Cancer Res. Gen. 1024	4.9

Normal Lung GENPAK 061010	17.7	Breast Cancer Clontech 9100266	9.4
83239 Lung Met to Muscle (ODO4286)	33.4	Breast NAT Clontech 9100265	5.8
83240 Muscle NAT (ODO4286)	3.0	Breast Cancer INVITROGEN A209073	19.2
84136 Lung Malignant Cancer (OD03126)	7.3	Breast NAT INVITROGEN A2090734	5.0
84137 Lung NAT (OD03126)	6.6	Normal Liver GENPAK 061009	0.6
84871 Lung Cancer (OD04404)	5.0	Liver Cancer GENPAK 064003	1.8
84872 Lung NAT (OD04404)	4.9	Liver Cancer Research Genetics RNA 1025	1.2
84875 Lung Cancer (OD04565)	4.2	Liver Cancer Research Genetics RNA 1026	4.7
84876 Lung NAT (OD04565)	4.2	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	1.1
85950 Lung Cancer (OD04237-01)	19.5	Paired Liver Tissue Research Genetics RNA 6004-N	2.1
85970 Lung NAT (OD04237-02)	8.7	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	4.5
83255 Ocular Mel Met to Liver (ODO4310)	2.7	Paired Liver Tissue Research Genetics RNA 6005-N	1.0
83256 Liver NAT (ODO4310)	2.1	Normal Bladder GENPAK 061001	19.6
84139 Melanoma Mets to Lung (OD04321)	8.0	Bladder Cancer Research Genetics RNA 1023	8.7
84138 Lung NAT (OD04321)	6.9	Bladder Cancer INVITROGEN A302173	16.5
Normal Kidney GENPAK 061008	2.6	87071 Bladder Cancer (OD04718-01)	20.3
83786 Kidney Ca, Nuclear grade 2 (OD04338)	7.9	87072 Bladder Normal Adjacent (OD04718-03)	10.1
83787 Kidney NAT (OD04338)	2.5	Normal Ovary Res. Gen	9.4
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	6.6	Ovarian Cancer GENPAK 064008	15.1
83789 Kidney NAT (OD04339)	1.4	87492 Ovary Cancer (OD04768-07)	7.1
83790 Kidney Ca, Clear cell type (OD04340)	6.9	87493 Ovary NAT (OD04768-08)	3.5
83791 Kidney NAT (OD04340)	3.9	Normal Stomach GENPAK 061017	4.7
83792 Kidney Ca, Nuclear grade 3 (OD04348)	18.2	Gastric Cancer Clontech 9060358	2.1
83793 Kidney NAT (OD04348)	3.6	NAT Stomach Clontech 9060359	17.7
87474 Kidney Cancer (OD04622-01)	10.8	Gastric Cancer Clontech 9060395	14.7
87475 Kidney NAT (OD04622-03)	1.2	NAT Stomach Clontech 9060394	22.7
85973 Kidney Cancer (OD04450-01)	6.0	Gastric Cancer Clontech 9060397	100.0
85974 Kidney NAT (OD04450-03)	1.9	NAT Stomach Clontech 9060396	14.8
Kidney Cancer Clontech 8120607	3.2	Gastric Cancer GENPAK 064005	32.3

Table 54. Panel 4D

	Relative Expression(%)	Tissue Name	Relative Expression(%)
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Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
93768_Secondary Th1_anti-CD28/anti-CD3	4dtm4244t_ ag2431	93100_HUVEC (Endothelial)_IL-1b	4dtm4244t_ ag2431
93769_Secondary Th2_anti-CD28/anti-CD3	69.7	93779_HUVEC (Endothelial)_IFN gamma	15.2
93770_Secondary Tr1_anti-CD28/anti-CD3	100.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	11.8
93573_Secondary Th1_resting day 4-6 in IL-2	65.5	93101_HUVEC (Endothelial)_TNF alpha + IL4	20.4
93572_Secondary Th2_resting day 4-6 in IL-2	50.0	93781_HUVEC (Endothelial)_IL-11	14.7
93571_Secondary Tr1_resting day 4-6 in IL-2	46.7	93583_Lung Microvascular Endothelial Cells_none	32.1
93568_primary Th1_anti-CD28/anti-CD3	92.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	38.2
93569_primary Th2_anti-CD28/anti-CD3	79.0	92662_Microvascular Dermal endothelium_none	41.2
93570_primary Tr1_anti-CD28/anti-CD3	57.0	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	34.9
93565_primary Th1_resting dy 4-6 in IL-2	80.1	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	51.8
93566_primary Th2_resting dy 4-6 in IL-2	61.6	93347_Small Airway Epithelium_none	18.8
93567_primary Tr1_resting dy 4-6 in IL-2	31.6	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	43.2
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	46.0	92668_Coronary Artery SMC_resting	30.8
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	40.1	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	20.7
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	29.5	93107_astrocytes_resting	11.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	33.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	11.2
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	38.4	92666_KU-812 (Basophil)_resting	9.7
93354_CD4_none	20.0	92667_KU-812 (Basophil)_PMA/ionomycin	18.9
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	49.3	93579_CCD1106 (Keratinocytes)_none	46.0
93103_LAK cells_resting	85.9	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	31.9
93788_LAK cells_IL-2	32.3	93791_Liver Cirrhosis	4.9
93787_LAK cells_IL-2+IL-12	24.1	93792_Lupus Kidney	2.6
93789_LAK cells_IL-2+IFN gamma	20.9	93577_NCI-H292	17.8
93790_LAK cells_IL-2+ IL-18	14.0	93358_NCI-H292_IL-4	15.1
93104_LAK cells_PMA/ionomycin and IL-18	36.3	93360_NCI-H292_IL-9	17.3

93578_NK Cells IL-2_resting	14.4	93359_NCI-H292_IL-13	5.0
93109_Mixed Lymphocyte Reaction_Two Way MLR	29.7	93357_NCI-H292_IFN gamma	13.5
93110_Mixed Lymphocyte Reaction_Two Way MLR	27.2	93777_HPAEC_-	14.3
93111_Mixed Lymphocyte Reaction_Two Way MLR	34.9	93778_HPAEC_IL-1 beta/TNA alpha	30.1
93112_Mononuclear Cells (PBMCs)_resting	16.6	93254_Normal Human Lung Fibroblast_none	39.8
93113_Mononuclear Cells (PBMCs)_PWM	36.6	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	38.7
93114_Mononuclear Cells (PBMCs)_PHA-L	35.4	93257_Normal Human Lung Fibroblast_IL-4	63.7
93249_Ramos (B cell)_none	11.8	93256_Normal Human Lung Fibroblast_IL-9	55.5
93250_Ramos (B cell)_ionomycin	13.7	93255_Normal Human Lung Fibroblast_IL-13	59.5
93349_B lymphocytes_PWM	25.5	93258_Normal Human Lung Fibroblast_IFN gamma	78.5
93350_B lymphocytes_CD40L and IL-4	10.8	93106_Dermal Fibroblasts CCD1070_resting	57.8
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	5.1	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	64.2
93248_EOL-1 (Eosinophil)_dbcAMP/PMA/ionomycin	15.6	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	27.2
93356_Dendritic Cells_none	33.4	93772_dermal fibroblast_IFN gamma	33.2
93355_Dendritic Cells_LPS 100 ng/ml	31.0	93771_dermal fibroblast_IL-4	38.2
93775_Dendritic Cells_anti-CD40	25.7	93260_IBD Colitis 2	4.0
93774_Monocytes_resting	29.9	93261_IBD Crohns	7.9
93776_Monocytes_LPS 50 ng/ml	14.4	735010_Colon_normal	35.1
93581_Macrophages_resting	28.3	735019_Lung_none	38.4
93582_Macrophages_LPS 100 ng/ml	35.1	64028-1_Thymus_none	18.7
93098_HUVEC (Endothelial)_none	28.1	64030-1_Kidney_none	52.1
93099_HUVEC (Endothelial)_starved	37.1		

Table 55. Panel CNS_neurodegeneration_v1.0

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm6902t_ag2431_b1s2		tm6902t_ag2431_b1s2
AD 1 Hippo	9.1	Control (Path) 3 Temporal Ctx	2.0
AD 2 Hippo	0.0	Control (Path) 4 Temporal Ctx	0.0
AD 3 Hippo	0.0	AD 1 Occipital Ctx	2.0
AD 4 Hippo	0.0	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	61.4	AD 3 Occipital Ctx	3.6

AD 6 Hippo	6.2	AD 4 Occipital Ctx	0.0
Control 2 Hippo	0.0	AD 5 Occipital Ctx	4.1
Control 4 Hippo	0.0	AD 6 Occipital Ctx	34.0
Control (Path) 3 Hippo	0.0	Control 1 Occipital Ctx	0.0
AD 1 Temporal Ctx	2.9	Control 2 Occipital Ctx	4.5
AD 2 Temporal Ctx	0.0	Control 3 Occipital Ctx	3.4
AD 3 Temporal Ctx	0.0	Control 4 Occipital Ctx	4.1
AD 4 Temporal Ctx	0.0	Control (Path) 1 Occipital Ctx	5.7
AD 5 Inf Temporal Ctx	52.5	Control (Path) 2 Occipital Ctx	2.1
AD 5 Sup Temporal Ctx	100.0	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	6.6	Control (Path) 4 Occipital Ctx	9.5
AD 6 Sup Temporal Ctx	16.6	Control 1 Parietal Ctx	0.0
Control 1 Temporal Ctx	0.0	Control 2 Parietal Ctx	61.0
Control 2 Temporal Ctx	1.7	Control 3 Parietal Ctx	1.3
Control 3 Temporal Ctx	1.3	Control (Path) 1 Parietal Ctx	13.6
Control 4 Temporal Ctx	0.0	Control (Path) 2 Parietal Ctx	0.0
Control (Path) 1 Temporal Ctx	6.6	Control (Path) 3 Parietal Ctx	3.1
Control (Path) 2 Temporal Ctx	7.4	Control (Path) 4 Parietal Ctx	1.4

Panel 1.3D Summary Ag2431 The NOV11 gene, a homolog of thymosin beta 10, is most highly expressed in the hippocampus (CT=24.2) and is expressed widely in the CNS. This gene appears to be important in the process of gliosis, which is a hallmark of all of the neurodegenerative diseases. Furthermore, the formation of a glial scar is one of the principle barriers to neuroregeneration in response to spinal cord injury and head trauma. Therefore, the selective down-regulation of this gene and/or its protein product may be beneficial in the treatment of spine or head injury, or in any of the neurodegenerative diseases (Alzheimer's, Parkinson's, Huntington's, spinocerebellar ataxia, etc).

The NOV11 gene also has moderate to low expression in many metabolic tissues including adipose, adrenal, adult and fetal heart, adult and fetal liver, adult and fetal skeletal muscle, pancreas, pituitary and thyroid. The gene appears to be expressed at higher levels in fetal skeletal muscle (CT=28) than in adult skeletal muscle (CT=31.7) and could potentially be used to distinguish between the adult and fetal phenotypes of this tissue. In addition, the greater expression in fetal skeletal muscle suggests that the NOV11 gene may play a role in muscular growth or development in the fetus and therefore could act in a regenerative capacity in an adult. Thus, therapeutic modulation of the NOV11 gene could be useful in the treatment of muscle related diseases and treatment with the protein product could restore muscle mass or function to weak or dystrophic muscle.

The NOV11 gene is expressed at significant levels in cell lines derived from breast cancer, liver cancer and melanoma when compared to expression in the corresponding normal tissues. Thus, the expression of this gene could be useful as a marker or as a therapeutic for breast and liver cancer, as well as melanomas. In addition, therapeutic modulation of the activity of the protein encoded by the NOV11 gene, through the use of peptides, antibodies, chimeric molecules or small molecule drugs, may be useful in the therapy of these cancers.

Panel 2D Summary Ag2431 Highest expression of the NOV11 gene is seen in a gastric cancer sample (CT=23.5). The expression of this gene in panel 2D shows an association with samples derived from ovarian, bladder, liver, breast, kidney and colon cancers when compared to the matched normal tissue. A lung cancer that has metastasized to muscle also shows increased expression of this gene when compared to the adjacent muscle tissue. Thus, expression of the NOV11 gene could be of use as a marker for these cancers. Furthermore, therapeutic modulation of the activity of the product of this gene, through the use of peptides, antibodies, chimeric molecules or small molecule drugs, may be beneficial in the treatment of these cancers.

Panel 4B Summary Ag2431 The NOV11 gene is ubiquitously expressed throughout this panel in both normal cell types and cell lines, regardless of their activation status. This gene encodes a protein that has homology with Thymosin beta-10. Some reports indicate that thymosin beta 10 (as thymosin beta 4- which is functionally very similar) is an effective regulator of a large subset of actin filaments in living cells. Reduced expression of thymosin beta-10 may contribute to the senescent phenotype by reducing EC plasticity and thus impairing their response to migratory stimuli. Therefore, therapeutics designed with the protein encoded for by the NOV11 gene may play a role in maintaining or restoring normal function of lymphoid, lung, dermal fibroblasts, endothelial cells and could be beneficial in preventing aging of the cells.

Panel CNS_neurodegeneration_v1.0 Summary Ag2431 Expression of the NOV11 gene is restricted to a few samples in this panel, with highest expression in the cerebral cortex of an Alzheimer's patient (CT=33.5). While no association between the expression of this gene and the presence of Alzheimer's disease is detected in this panel, these results confirm the expression of this gene in the brains of a further set of individuals. Please see Panel 1.3D for a discussion of potential utility of this gene in the central nervous system (Carpintero et al., Expression of the thymosin beta10 gene in normal and kainic acid-treated rat forebrain. Brain Res Mol Brain Res. 70:141-6, 1999).

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims.